
N O T E S
(TW)

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MPSrch_DP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:11:19 1998; Maspar time 3.79 Seconds
Tabular output not generated. 111.077 Million cell updates/sec

Title: >US-08-817-547A-31
Description: (1-10) from US08817547A.pep
Perfect Score: 73
Sequence: 1 LRRKLODVHN 10

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: spltemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 24.067; Variance 30.335; scale 0.793

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	63	86.3	105	10	063473	PARATHYROID HORMONE (F	2.77e+02
2	54	74.0	400	3	026648	TEKTIN B1.	2.35e+00
3	54	74.0	735	0	017750	C06G3.9 PROTEIN.	2.35e+00
4	53	72.6	398	8	004471	SIMILAR TO SACCCHAROMYC	3.74e+00
5	52	71.2	485	3	016873	C13A2.5 PROTEIN.	5.94e+00
6	52	71.2	929	9	032491	PUTATIVE NG-ADEININE S	5.94e+00
7	52	71.2	1312	2	092878	RAD50.	5.94e+00
8	52	71.2	2475	11	008358	POLYPROTEIN PP220.	5.94e+00
9	51	69.9	242	8	P93468	MADS-BOX FAMILY TRANSC	9.37e+00
10	51	69.9	242	8	040970	PUTATIVE MADS-BOX FAMI	9.37e+00
11	51	69.9	257	8	040700	BOX PROTEIN.	9.37e+00
12	51	69.9	317	4	019037	MCL-R PROTEIN.	9.37e+00
13	51	69.9	317	4	P79328	MELANOCYTE STIMULATING	9.37e+00
14	51	69.9	385	3	017076	C38G3.3 PROTEIN.	9.37e+00
15	51	69.9	733	3	024250	TARTAN PROTEIN PRECURS	9.37e+00
16	51	69.9	1200	9	P73340	CHROMOSOME SEGREGATION	9.37e+00
17	51	69.9	1648	2	015058	MRNA (K1A0042) FOR OR	1.47e+01
18	50	68.5	279	10	063338	MYOSIN HEAVY CHAIN (AA	1.47e+01
19	50	68.5	334	3	017970	C1A010.1.	1.47e+01
20	50	68.5	360	9	034130	HISC.	1.47e+01

21	50	68.5	621	10	063339	MYOSIN HEAVY CHAIN 21	1.47e+01
22	50	68.5	1938	10	008639	MYOSIN.	1.47e+01
23	50	68.5	1972	10	008638	MYOSIN.	1.47e+01
24	49	67.1	257	9	044871	PLASMIN, ORFA, B, C, D	2.29e+01
25	49	67.1	899	1	006132	CHROMOSOME XII COSMID	2.29e+01
26	49	67.1	991	2	014844	MYOSIN LIGHT CHAIN KIN	2.29e+01
27	49	67.1	1583	2	015045	K1A00336.	2.29e+01
28	49	67.1	1914	2	015746	MYOSIN LIGHT CHAIN KIN	2.29e+01
29	49	67.1	3212	3	094010	HYPOHEMICAL 15.4 KD P	3.54e+01
30	48	65.8	133	9	P73917	T08G11.1.	3.54e+01
31	48	65.8	164	9	P66113	POLYPEPTIDE DEFORMYLAS	3.54e+01
32	48	65.8	400	2	000328	HUNTINGTIN INTERACTING	3.54e+01
33	48	65.8	481	3	018253	COSMID C27D9.	3.54e+01
34	48	65.8	914	2	000291	HUNTINGTIN INTERACTING	3.54e+01
35	48	65.8	943	2	030320	ATP-DEPENDENT RNA HELI	3.54e+01
36	48	65.8	951	2	045227	K1A0291 (FRAGMENT).	3.54e+01
37	48	65.8	1034	3	017117	M151.4 PROTEIN.	3.54e+01
38	48	65.8	1038	1	012532	HYPOHEMICAL 119.1 KD	3.54e+01
39	48	65.8	1091	3	018082	SIMILARITY TO MYOSIN H	3.54e+01
40	48	65.8	1459	3	021874	R08E10.5.	3.54e+01
41	48	65.8	1625	8	008367	ACETYL-COA CARBOXYLASE	3.54e+01
42	48	65.8	2024	2	015154	PERICENTRIOL MATERIAL	3.54e+01
43	48	65.8	2325	8	041743	ACETYL-COENZYME A CARB	3.54e+01
44	48	65.8	2346	3	001385	TPR HOMOLOG.	3.54e+01
45	48	65.8	2510	3	094658	EXPORTED SERINE/THREON	3.54e+01

ALIGNMENTS

RESULT	ID	063473	PRELIMINARY:	PRT:	105 AA.
AC	063473;				
DT	01-NOV-1996 (TREMBREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE (FRAGMENT).				
CS	NR.				
GN	RATTUS NORVEGICUS (RAT).				
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUDAROTA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-THYROID, AND PARATHYROID;				
RA	SCHMELZER H.J., GROSS G., MAYER H.;				
RL	ADV. GENE TECHNOL. 21:228-229(1984).				
DR	EMBL; M54875; G601933; -.				
FT	NON TER				
SO	SEQUENCE	105 AA;	11746 MW;	6AC3163E CRC32;	
Query Match		86.3%;	Score 63;	DB 10;	Length 105;
Best Local Similarity		90.0%;	Pred. No. 2.77e-02;		
Matches	9;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;		
DB	45 LRRKLODVHN 54				
OY	1 LRRKLODVHN 10				
RESULT	2	PRELIMINARY:	PRT:	400 AA.	
AC	026648;				
DT	01-NOV-1996 (TREMBREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1996 (TREMBREL. 01, LAST ANNOTATION UPDATE)				
DE	TEKTIN B1.				
CS	STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).				
OC	EUDAROTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;				
OC	EUDAROTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;				
EDUCHINOIDEA.					
EN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-EMBRYO;				
RK	MEDLINE; 94140942.				
RA	CHEN R., PERRONE C.A., AMOS L.A., LINCK R.W.;				

RL J. CELL SCI. 106:909-918(1993).
 DR EMBL: L21838: G474949;
 SQ SEQUENCE 400 AA; 46147 MW; 75400E80 CRC32;
 Query Match 74.0%; Score 54; DB 3; Length 400;
 Best Local Similarity 80.0%;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 325 LERKLODAHN 334
 QY 1 LRRKLODVHN 10

Search completed: Thu Jul 30 11:11:48 1998
 Job time : 29 secs.

MIPS

(TW)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:00:59 1998; Maspar time 4.06 Seconds
Molecular output not generated. 83.029 Million cell updates/sec

Title: >US-08-817-547A-3
Description: (1-8) from US08817547A.pep
Perfect Score: 54
Sequence: 1 SVSEIOLM 8

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: splitemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.157; Variance 18.924; scale 1.118

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	50	92.6	105	10	063473	PARATHYROID HORMONE (F	5.43e-02
2	45	83.3	1405	10	P70366	STERIOD RECEPTOR COACT	1.44e+00
3	45	83.3	1405	10	061202	STERIOD RECEPTOR COACT	1.44e+00
4	45	83.3	1441	2	000150	STERIOD RECEPTOR COACT	1.44e+00
5	45	83.3	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	1.44e+00
6	44	81.5	248	9	008320	ACETYLGLUTAMATE KINASE	2.68e+00
7	43	79.6	167	9	P66578	YDAE PROTEIN.	4.96e+00
8	43	79.6	910	11	011421	HEXON PROTEIN.	4.96e+00
9	43	79.6	911	11	083905	TERMINAL PROTEIN.	4.96e+00
10	42	77.8	418	3	026662	VERY EARLY BLASTULA PR	9.08e+00
11	41	75.9	248	8	004682	PT16.	1.64e+01
12	41	75.9	276	3	021966	SIMILAR TO TYROSINE KI	1.64e+01
13	41	75.9	373	9	049979	CORA.	1.64e+01
14	41	75.9	481	10	060823	THYMOMA VIRAL PROTO-ON	1.64e+01
15	41	75.9	591	2	013026	65 KDA HYDROPHOBIC PRO	1.64e+01
16	41	75.9	591	2	000553	FOLATE CARRIER.	1.64e+01
17	41	75.9	896	9	055544	HYPOTHETICAL 100.3 KD	1.64e+01
18	41	75.9	1371	9	P73337	SENSORY TRANSDUCTION H	1.64e+01
19	41	75.9	3456	11	P89201	POLYPROTEIN.	1.64e+01
20	40	74.1	99	9	Q58911	HYPOTHETICAL 11.5 KD P	2.93e+01

21	40	74.1	189	3	019478	F15B9.1.	2.93e+01
22	40	74.1 <td>313</td> <td>3<td>002074</td><td>SIMILAR TO MYOSIN HEAV</td><td>2.93e+01</td></td>	313	3 <td>002074</td> <td>SIMILAR TO MYOSIN HEAV</td> <td>2.93e+01</td>	002074	SIMILAR TO MYOSIN HEAV	2.93e+01
23	40	74.1 <td>353</td> <td>9<td>034472</td><td>YRRI PROTEIN.</td><td>2.93e+01</td></td>	353	9 <td>034472</td> <td>YRRI PROTEIN.</td> <td>2.93e+01</td>	034472	YRRI PROTEIN.	2.93e+01
24	40	74.1 <td>394</td> <td>9<td>006164</td><td>MMGC.</td><td>2.93e+01</td></td>	394	9 <td>006164</td> <td>MMGC.</td> <td>2.93e+01</td>	006164	MMGC.	2.93e+01
25	40	74.1 <td>611</td> <td>3</td> <td>027063</td> <td>SIALIDASE (FRAGMENT).</td> <td>2.93e+01</td>	611	3	027063	SIALIDASE (FRAGMENT).	2.93e+01
26	40	74.1 <td>649</td> <td>3</td> <td>027064</td> <td>SIALIDASE.</td> <td>2.93e+01</td>	649	3	027064	SIALIDASE.	2.93e+01
27	40	74.1 <td>883</td> <td>3</td> <td>007995</td> <td>RNA-DIRECTED DNA POLYM</td> <td>2.93e+01</td>	883	3	007995	RNA-DIRECTED DNA POLYM	2.93e+01
28	40	74.1 <td>1150</td> <td>1</td> <td>002511</td> <td>HYPOTHETICAL 133.0 KD</td> <td>2.93e+01</td>	1150	1	002511	HYPOTHETICAL 133.0 KD	2.93e+01
29	40	74.1 <td>1710</td> <td>3</td> <td>019285</td> <td>HYPOTHETICAL PROTEIN F</td> <td>2.93e+01</td>	1710	3	019285	HYPOTHETICAL PROTEIN F	2.93e+01
30	40	74.1 <td>2668</td> <td>3</td> <td>020456</td> <td>F46C3.3.</td> <td>2.93e+01</td>	2668	3	020456	F46C3.3.	2.93e+01
31	39	72.2	155	9	060482	CGRR-RECEPTOR COMPONEN	5.17e+01
32	39	72.2	172	12	002529	B1549.F2.87.	5.17e+01
33	39	72.2	174	12	002529	FIBROBLAST GROWTH FACT	5.17e+01
34	39	72.2	174	12	002529	FIBROBLAST GROWTH FACT	5.17e+01
35	39	72.2	316	3	017822	F17A2.9.	5.17e+01
36	39	72.2	364	3	019506	COSMID ZC196.	5.17e+01
37	39	72.2	374	3	001625	COSMID ZC196.	5.17e+01
38	39	72.2	487	3	017179	COSMID ZC196.	5.17e+01
39	39	72.2	818	12	091742	FIBROBLAST GROWTH FACT	5.17e+01
40	39	72.2	822	12	091288	FIBROBLAST GROWTH FACT	5.17e+01
41	39	72.2	828	12	091743	FIBROBLAST GROWTH FACT	5.17e+01
42	39	72.2	922	12	090413	FIBROBLAST GROWTH FACT	5.17e+01
43	39	72.2	1645	3	027448	GLUTAMINE-DEPENDENT CA	5.17e+01
44	39	72.2	1810	3	018038	CODED FOR BY C. ELEGAN	5.17e+01
45	39	72.2	2489	1	006116	CHROMOSOME XVI COSMID	5.17e+01

ALIGNMENTS

RESULT	ID	Score	Length	DB	ID	Description	Pred. No.
1	063473	92.6%	105	10	063473	PARATHYROID HORMONE (F	5.43e-02
2	063473	83.3%	1405	10	P70366	STERIOD RECEPTOR COACT	1.44e+00
3	063473	83.3%	1405	10	061202	STERIOD RECEPTOR COACT	1.44e+00
4	063473	83.3%	1441	2	000150	STERIOD RECEPTOR COACT	1.44e+00
5	063473	83.3%	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	1.44e+00
6	063473	81.5%	248	9	008320	ACETYLGLUTAMATE KINASE	2.68e+00
7	063473	79.6%	167	9	P66578	YDAE PROTEIN.	4.96e+00
8	063473	79.6%	910	11	011421	HEXON PROTEIN.	4.96e+00
9	063473	79.6%	911	11	083905	TERMINAL PROTEIN.	4.96e+00
10	063473	77.8%	418	3	026662	VERY EARLY BLASTULA PR	9.08e+00
11	063473	75.9%	248	8	004682	PT16.	1.64e+01
12	063473	75.9%	276	3	021966	SIMILAR TO TYROSINE KI	1.64e+01
13	063473	75.9%	373	9	049979	CORA.	1.64e+01
14	063473	75.9%	481	10	060823	THYMOMA VIRAL PROTO-ON	1.64e+01
15	063473	75.9%	591	2	013026	65 KDA HYDROPHOBIC PRO	1.64e+01
16	063473	75.9%	591	2	000553	FOLATE CARRIER.	1.64e+01
17	063473	75.9%	896	9	055544	HYPOTHETICAL 100.3 KD	1.64e+01
18	063473	75.9%	1371	9	P73337	SENSORY TRANSDUCTION H	1.64e+01
19	063473	75.9%	3456	11	P89201	POLYPROTEIN.	1.64e+01
20	063473	74.1%	99	9	Q58911	HYPOTHETICAL 11.5 KD P	2.93e+01

Thu Jul 30 13:38:11 1998

US-08-817-547A-3.rsp

Page 2

DR EMBL; U64828; G1490876; -
SQ SEQUENCE 1405 AA; 152644 MW; 1743E755 CRC32;

Query Match

Best Local Similarity 83.38; Score 45; DB 10; Length 1405;
Matches 5; Conservatve 2; Mismatches 1; Indels 0; Gaps 0;

Db 73 TVDQIQIM 80

OY 1 SVSEIQIM 8

Search completed: Thu Jul 30 10:01:39 1998
Job time : 40 secs.

CC removal on an iminobiotin column followed by chromatography on a
 CC fractogel and reverse phase HPLC.
 SQ Sequence 16 AA;

Query Match 100.0%; Score 43; DB 25; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.43e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 10 svseql 16
 |||||
 OY 1 SVSEIQL 7

RESULT 2

ID W21947 standard; Protein; 20 AA.

AC W21947;

DT 30-JAN-1998 (first entry)

DE Fusion protein comprising linker and PTH 1-37 (residues 1-7).

Linker: parathyroid hormone 1-37; PTH 1-37; streptavidin;
 fusion protein; recombinant production; thrombin.

Synthetic.

OS Homo sapiens.

FH Key

FT Peptide

Location/Qualifiers

FT Peptide

FT Peptide

/note= "Met(13-139) streptavidin residue"

FT Peptide

FT Peptide

/note= "linker cleavable by thrombin"

FT Peptide

FT Peptide

/note= "parathyroid hormone 1-37 (residues 1-7)"

PN WO9718314-A1.

PD 22-MAY-1997.

PF 06-NOV-1996; E04850.

PR 16-NOV-1995; DE-042702.

PA (BOE) BOEHRINGER MANNHEIM GMBH.

PI Kopetzki E;

DR WPI: 97-289290/26.

DR N-PSDB: T73911.

PT Recombinant production of peptide(s) as fusions with streptavidin

PT attached via cleavable linker - especially for urotropin and

PT parathyroid hormone production

PS Example 3; Fig 3; 37pp; German.

CC The DNA encoding the present sequence, a linker and residues 1-7 of

CC the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage

CC optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII

CC (SA) sequence, to give PSA-THRO-PTH. PSA-THRO-PTH and the LacIq

CC repressor plasmid PUBS500 were used to transform E. coli K12 RM82.

CC The transformants were grown, with IPTG induction, in medium

CC containing kanamycin and ampicillin. Cells were harvested, lysed

CC and isolated inclusion bodies solubilised in guanidine

CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer.

CC The solution was clarified and the supernatant concentrated and

CC material was incubated with thrombin and the PTH 1-37 fragment

CC released, recovered by SA fragment removal on an iminobiotin

CC column followed by chromatography on a fractogel and reverse phase

CC HPLC.

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Search completed: Thu Jul 30 10:05:25 1998
 Job time : 16 secs.

SQ Sequence 20 AA;

Query Match

Best Local Similarity 100.0%; Score 43; DB 25; Length 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 14 svseql 20
 |||||
 OY 1 SVSEIQL 7

M P S E R E L E I (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:04:35 1998; Maspar time 3.05 Seconds
Molecular output not generated. 83.806 Million cell updates/sec

Title: >US-08-817-547A-4
Description: (1-7) from US08817547A.pep
Perfect Score: 43
Sequence: 1 SVSEIQL 7

Scoring table:
PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 19.518; Variance 19.793; scale 0.986

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	43	100.0	34	5	1H7H cyclic parathyroid ho	2.97e+00
2	43	100.0	34	5	12WA parathyroid hormone	2.97e+00
3	43	100.0	37	5	1HPR parathyroid hormone f	2.97e+00
4	43	100.0	115	1	PTBG parathyroid hormone p	2.97e+00
5	43	100.0	115	1	PTHG parathyroid hormone p	2.97e+00
6	41	95.3	115	2	A05091 parathyroid hormone p	9.26e+00
7	41	95.3	896	2	S76064 parathyroid hormone	9.26e+00
8	41	95.3	896	2	S59990 parathyroid hormone	9.26e+00
9	39	90.7	36	5	12WB parathyroid hormone	2.77e+01
10	39	90.7	105	2	151851 parathyroid hormone	2.77e+01
11	39	90.7	567	2	C69611 ABC transporter regul	2.77e+01
12	39	90.7	1827	2	A35694 cutl protein - f1ssio	4.72e+01
13	38	88.4	119	2	A34937 parathyroid hormone p	4.72e+01
14	38	88.4	958	2	S47179 parathyroid hormone p	4.72e+01
15	38	88.4	3124	2	A40020 collagen alpha 1(XII)	4.72e+01
16	37	86.0	312	2	S66952 hypothetical protein	7.96e+01
17	37	86.0	407	2	B64311 collagenase p1tc homo	7.96e+01
18	37	86.0	436	5	3MINA2 nitrogennase (EC 1.18.	7.96e+01
19	37	86.0	436	5	2MINA2 nitrogennase (EC 1.18.	7.96e+01
20	37	86.0	437	5	1MINC2 nitrogennase (EC 1.18.	7.96e+01
21	37	86.0	437	5	3MINC2 nitrogennase (EC 1.18.	7.96e+01
22	37	86.0	437	5	2MINC2 nitrogennase (EC 1.18.	7.96e+01
23	37	86.0	437	5	1MINA2 nitrogennase (EC 1.18.	7.96e+01

24	37	86.0	438	2	A55070	DNA primase (EC 2.7.7	7.96e+01
25	37	86.0 <td>478<th>5</th><th>1N2CC</th><th>nitrogennase molybdenu</th><th>7.96e+01</th></td>	478 <th>5</th> <th>1N2CC</th> <th>nitrogennase molybdenu</th> <th>7.96e+01</th>	5	1N2CC	nitrogennase molybdenu	7.96e+01
26	37	86.0 <td>478<th>5</th><th>1N2WA</th><th>nitrogennase molybdenu</th><th>7.96e+01</th></td>	478 <th>5</th> <th>1N2WA</th> <th>nitrogennase molybdenu</th> <th>7.96e+01</th>	5	1N2WA	nitrogennase molybdenu	7.96e+01
27	37	86.0 <td>492<th>1</th><th>NIWMA</th><th>nitrogennase (EC 1.18.</th><th>7.96e+01</th></td>	492 <th>1</th> <th>NIWMA</th> <th>nitrogennase (EC 1.18.</th> <th>7.96e+01</th>	1	NIWMA	nitrogennase (EC 1.18.	7.96e+01
28	37	86.0 <td>605<th>2</th><th>S36592</th><th>El protein - human pa</th><th>7.96e+01</th></td>	605 <th>2</th> <th>S36592</th> <th>El protein - human pa</th> <th>7.96e+01</th>	2	S36592	El protein - human pa	7.96e+01
29	37	86.0 <td>615<th>2</th><th>A05269</th><th>collagen alpha 1(III)</th><th>7.96e+01</th></td>	615 <th>2</th> <th>A05269</th> <th>collagen alpha 1(III)</th> <th>7.96e+01</th>	2	A05269	collagen alpha 1(III)	7.96e+01
30	37	86.0 <td>764<th>2</th><th>A49448</th><th>irregular chiasm C-to</th><th>7.96e+01</th></td>	764 <th>2</th> <th>A49448</th> <th>irregular chiasm C-to</th> <th>7.96e+01</th>	2	A49448	irregular chiasm C-to	7.96e+01
31	37	86.0 <td>1116<th>2</th><th>S41915</th><th>DNA-directed RNA poly</th><th>7.96e+01</th></td>	1116 <th>2</th> <th>S41915</th> <th>DNA-directed RNA poly</th> <th>7.96e+01</th>	2	S41915	DNA-directed RNA poly	7.96e+01
32	37	86.0 <td>1132<th>2</th><th>JC4127</th><th>protein-tyrosine kina</th><th>7.96e+01</th></td>	1132 <th>2</th> <th>JC4127</th> <th>protein-tyrosine kina</th> <th>7.96e+01</th>	2	JC4127	protein-tyrosine kina	7.96e+01
33	36	83.7 <td>115<th>2</th><th>JC4202</th><th>parathyroid hormone -</th><th>1.32e+02</th></td>	115 <th>2</th> <th>JC4202</th> <th>parathyroid hormone -</th> <th>1.32e+02</th>	2	JC4202	parathyroid hormone -	1.32e+02
34	36	83.7 <td>116<th>2</th><th>S22553</th><th>Ig heavy chain V regl</th><th>1.32e+02</th></td>	116 <th>2</th> <th>S22553</th> <th>Ig heavy chain V regl</th> <th>1.32e+02</th>	2	S22553	Ig heavy chain V regl	1.32e+02
35	36	83.7 <td>335<th>2</th><th>S35126</th><th>anthranilate phosphor</th><th>1.32e+02</th></td>	335 <th>2</th> <th>S35126</th> <th>anthranilate phosphor</th> <th>1.32e+02</th>	2	S35126	anthranilate phosphor	1.32e+02
36	36	83.7 <td>350<th>2</th><th>B39364</th><th>GDE-1 embryonic growt</th><th>1.32e+02</th></td>	350 <th>2</th> <th>B39364</th> <th>GDE-1 embryonic growt</th> <th>1.32e+02</th>	2	B39364	GDE-1 embryonic growt	1.32e+02
37	36	83.7 <td>366<th>2</th><th>139518</th><th>lipoprotein - Actinob</th><th>1.32e+02</th></td>	366 <th>2</th> <th>139518</th> <th>lipoprotein - Actinob</th> <th>1.32e+02</th>	2	139518	lipoprotein - Actinob	1.32e+02
38	36	83.7 <td>367<th>2</th><th>139649</th><th>lipoprotein - Actinob</th><th>1.32e+02</th></td>	367 <th>2</th> <th>139649</th> <th>lipoprotein - Actinob</th> <th>1.32e+02</th>	2	139649	lipoprotein - Actinob	1.32e+02
39	36	83.7 <td>372<th>2</th><th>D64716</th><th>regulatory protein Dn</th><th>1.32e+02</th></td>	372 <th>2</th> <th>D64716</th> <th>regulatory protein Dn</th> <th>1.32e+02</th>	2	D64716	regulatory protein Dn	1.32e+02
40	36	83.7 <td>381<th>2</th><th>S65212</th><th>hypothetical protein</th><th>1.32e+02</th></td>	381 <th>2</th> <th>S65212</th> <th>hypothetical protein</th> <th>1.32e+02</th>	2	S65212	hypothetical protein	1.32e+02
41	36	83.7 <td>399<th>2</th><th>E33282</th><th>gene-binding protein (</th><th>1.32e+02</th></td>	399 <th>2</th> <th>E33282</th> <th>gene-binding protein (</th> <th>1.32e+02</th>	2	E33282	gene-binding protein (1.32e+02
42	36	83.7 <td>553<th>1</th><th>G1BPSV</th><th>gene I protein - spir</th><th>1.32e+02</th></td>	553 <th>1</th> <th>G1BPSV</th> <th>gene I protein - spir</th> <th>1.32e+02</th>	1	G1BPSV	gene I protein - spir	1.32e+02
43	36	83.7 <td>989<th>2</th><th>156333</th><th>apolipoprotein B - ra</th><th>1.32e+02</th></td>	989 <th>2</th> <th>156333</th> <th>apolipoprotein B - ra</th> <th>1.32e+02</th>	2	156333	apolipoprotein B - ra	1.32e+02
44	36	83.7 <td>1070<th>2</th><th>A54600</th><th>phosphatidylinositol</th><th>1.32e+02</th></td>	1070 <th>2</th> <th>A54600</th> <th>phosphatidylinositol</th> <th>1.32e+02</th>	2	A54600	phosphatidylinositol	1.32e+02
45	36	83.7 <td>1150<th>2</th><th>S49956</th><th>probable membrane pro</th><th>1.32e+02</th></td>	1150 <th>2</th> <th>S49956</th> <th>probable membrane pro</th> <th>1.32e+02</th>	2	S49956	probable membrane pro	1.32e+02

ALIGNMENTS

RESULT	ENTRY	1	1H7H	#type complete
TITLE			cyclic parathyroid hormone residues 1-34 mutant M8NLE,	
PDB-TITLE			K130RN, S17E, M18NLE - synthetic	
			the solution structure of cyclic human parathyroid hormone	
			fragment 1 - 34, NMR, 10 structures	

ORGANISM	REFERENCE	#formal_name synthetic
A68105		

#authors	Roesch, P.; Seidel, G.; Schaefer, W.; Esswein, A.; Hofmann, E.
----------	--

#substssn	submitted to the Brookhaven Protein Data Bank, April 1997
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#cross-references	PDB:1H7H
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COMMENT	Resolution: not applicable
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COMMENT	Determination: NMR
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KEYWORDS	cyclic; human parathyroid hormone; norleucine NMR structure; ornithine
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FEATURE	#region helix (right hand 3-10)\
4-6	#region helix (right hand alpha)

SUMMARY	#length 34 #molecular-weight 4146 #checksum 5768
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Query Match	100.0%; Score 43; DB 5; Length 34;
Best Local Similarity <th>100.0%; Pred. No. 2.97e+00;</th>	100.0%; Pred. No. 2.97e+00;
Matches <th>7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</th>	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	1 SVSEIQL 7
QY <th>1 SVSEIQL 7</th>	1 SVSEIQL 7

RESULT	2	12WA	#type complete
ENTRY			parathyroid hormone (residues 1-34) - human
TITLE			HPTH(1-34)
ALTERNATE_NAMES			structure of human parathyroid hormone fragment 1-34, NMR 10
PDB-TITLE			structures

ORGANISM	#formal_name Homo sapiens #common_name man
REFERENCE	A67856
#authors	Roesch, P.; Marx, U.C.
#submitors	submitted to the Brookhaven Protein Data Bank, June 1996

#cross-references	PDB:12WA
REFERENCE	IN001717
#authors	Marx, U.C.

COMMENT	in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT <th>Resolution: not applicable</th>	Resolution: not applicable
COMMENT <th>Determination: NMR</th>	Determination: NMR

KEYWORDS hormone
 FEATURE 6-9
 19-30
 SUMMARY #region helix (right hand alpha) \
 #region helix (right hand alpha) \
 #length 34 #molecular-weight 418 #checksum 5629
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 Best Local Similarity 100.0%; Pred. No. 2.97e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 SYSSEQ 7
 111111
 QY 1 SYSSEQ 7

Search completed: Thu Jul 30 10:04:51 1998
 Job time : 16 secs.

MISSED

(TW)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:03:18 1998; MasPar time 2.05 Seconds
85.496 Million cell updates/sec
Abular output not generated.

Title: >US-08-817-547A-4
Description: (1-7) from US08817547A.dep
Perfect Score: 43
Sequence: 1 SVSEIOL 7

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prots35
1:swlssl

Statistics: Mean 20.233; Variance 16.121; scale 1.255

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	43	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	3.67e-01
2	43	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	3.67e-01
3	41	95.3	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.46e+00
4	41	95.3	896	1	APCE_SYNY4 PHYCOBILISOME 100.5 KD	5.55e+00
5	39	90.7	567	1	CYDC_BACSU TRANSPORT ATP-BINDING	5.55e+00
6	39	90.7	1827	1	CUT1_SCHRO CUT1 PROTEIN.	5.55e+00
7	38	88.4	119	1	PTHY_CHICK PARATHYROID HORMONE PR	1.06e+01
8	38	88.4	3124	1	CAIC_CHICK COLLAGEN ALPHA 1(XII)	1.06e+01
9	37	86.0	407	1	YO90_METJA PUTATIVE PROTEASE M100	1.98e+01
10	37	86.0	438	1	PR11_DROME DNA PRIMASE 50 KD SUBU	1.98e+01
11	37	86.0	491	1	NIFD_AZOVI NITROGENASE MOLYBDENUM	1.98e+01
12	37	86.0	605	1	VEI_HPV09 REPLICATION PROTEIN E1	1.98e+01
13	37	86.0	615	1	CA13_CHICK COLLAGEN ALPHA 1(I)(I)	1.98e+01
14	37	86.0	675	1	VP55_YEAST VACUOLAR PROTEIN SORTI	1.98e+01
15	37	86.0	764	1	ICCR_DROME IRREGULAR CHISM C-ROU	1.98e+01
16	37	86.0	1116	1	RPOB_HETCA DNA-DIRECTED RNA POLYM	1.98e+01
17	37	86.0	1132	1	JAK2_RAT TYROSINE-PROTEIN KINAS	1.98e+01
18	37	86.0	1145	1	DPOG_DROME DNA POLYMERASE GAMMA (1.98e+01
19	36	83.7	115	1	PTHY_CANFA PARATHYROID HORMONE PR	3.66e+01
20	36	83.7	282	1	DAAA_STAHA D-ALANINE AMINOTRANSF	3.66e+01
21	36	83.7	335	1	TRPD_LACUA ANTHRANILATE PHOSPHORI	3.66e+01
22	36	83.7	350	1	UOG1_MOUSE HYPOTHETICAL UOG-1 PRO	3.66e+01
23	36	83.7	392	1	HRC2_CHLTR HEAT-INDUCIBLE TRANSCR	3.66e+01

RESULT	ID	PTHY_HUMAN	STANDARD	PTH	ALIGNMENTS
24	36	83.7	393	1	THIL_RHME ACETYL-COA ACETYLTRANS
25	36	83.7	537	1	Z029_XENLA OOCYTE ZINC FINGER PRO
26	36	83.7	553	1	VG1_SPV4 CAPSID PROTEIN.
27	36	83.7	832	1	KLPI1_SCHPO KINESIN-LIKE PROTEIN 1
28	36	83.7	857	1	CLPB_ECOLI CLPB PROTEIN (HEAT SHO
29	36	83.7	859	1	YOD3_CAEEL HYPOTHETICAL 96.7 KD P
30	36	83.7	1047	1	YBDE_ECOLI HYPOTHETICAL 114.7 KD
31	36	83.7	1070	1	PI1B_HUMAN PHOSPHATIDYLINOSITOL 3
32	36	83.7	1150	1	YVIC_YEAST HYPOTHETICAL 133.0 KD
33	35	81.4	262	1	FLGG_CAUCR FLAGELLAR BASAL-BODY R
34	35	81.4	303	1	Y367_HAEIN HYPOTHETICAL PROTEIN H
35	35	81.4	314	1	REPE_STANU REPLICATION INITIATION
36	35	81.4	325	1	STK3_ECOLI HYPOTHETICAL LYSYL-TRN
37	35	81.4	464	1	WCAM_ECOLI COLANIC ACID BIOSYNTH
38	35	81.4	500	1	ZIPP_DROME ZIPPER PROTEIN PRECURS
39	35	81.4	679	1	PBP2_STREN PENICILLIN-BINDING PRO
40	35	81.4	760	1	YCE5_YEAST HYPOTHETICAL 87.2 KD P
41	35	81.4	853	1	PXA2_YEAST PEROXISOMAL LONG-CHAIN
42	35	81.4	890	1	YOUN_ECOLI PROBABLE SENSOR PROTEI
43	35	81.4	1036	1	P200_MYCPN INTEGRIN ALPHA-E PRECU
44	35	81.4	1167	1	ITAE_MOUSE RNA POLYMERASE BETA SU
45	35	81.4	2109	1	RRPL_VSVSJ

RESULT 1
ID PTHY_HUMAN STANDARD; PTH; 115 AA.
AC P01270;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82150870.
RA HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83169834.
RA VASICER T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J.,
RA HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).
RN [3]
RP SEQUENCE OF 26-37.
RX MEDLINE; 74174967.
RA JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;
RL NATURE 249:155-157(1974).
RN [4]
RP SEQUENCE OF 32-68.
RX MEDLINE; 7411656.
RA NIALL H.D., SAUER R.T., JACOBS J.W., KUTTMANN H.T., SEGRE G.V.,
RA O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T. JR.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).
RN [5]
RP SEQUENCE OF 61-83 AND 84-115.
RX MEDLINE; 79082855.
RA KUTTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,
RA POTTS J.T. JR.;
RL BIOCHEMISTRY 17:5723-5729(1978).
RN [6]
RP SEQUENCE OF 75-100.
RA KUTTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,
RA O'RIORDAN J.L.H., POTTS J.T. JR.;
RL (IN) CALCIUM-REGULATING HORMONES. TALMADGE R.V., OWEN M.,
PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,
(1975).
RN [7]

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN (8)
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGEAR G.W., VAN RIETSCHOEN J., GREEN E., NIALL H.D.,
 RL KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RN HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDREATTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RL RINKER B., RITTEL W., SIEBER P.;
 RN HEV. CHIM. ACTA 56:470-473(1973).
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAVUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN (11)
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345518.
 RA BARDEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN (12)
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MAXX U.C., AUSTRERMAN S., BAYER P., ADERMAN K., EJCART A.,
 RL STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSMANN W.-G.,
 RN ROSCH P.;
 RA J. BIOL. CHEM. 270:15194-15202(1995).
 RN (13)
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RL KRONENBERG H.M.;
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 DR EMBL: J00301; G190704; -.
 DR EMBL: V00597; G37144; -.
 DR EMBL: A28146; E186700; -.
 DR PIR: A01536; PTHU.
 DR PIR: A19339; A19339.
 DR PDB: 1HPH; 10-JUL-95.
 DR PDB: 1HTH; 15-OCT-97.
 DR PDB: 1ZNA; 12-MAR-97.
 DR PDB: 1ZMB; 12-MAR-97.
 DR PDB: 1ZMC; 12-MAR-97.
 DR PDB: 1ZMD; 12-MAR-97.
 DR PDB: 1ZME; 12-MAR-97.
 DR PDB: 1ZWF; 16-JUN-97.
 DR PDB: 1ZNG; 16-JUN-97.
 DR MIM: 146200; -.
 DR MIM: 168450; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPER 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA; 12861 MW; 243E87C7 CRC32;
 SQ

Query Match 100.0%; Score 43; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 3.67e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 SVSEIOL 38
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 QY 1 SVSEIOL 7

RESULT 2
 ID PTH_PIG STANDARD; PRT; 115 AA.
 AC P01269;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; ARTIODACTYLA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87316938.
 RA SCHMELZER H.-J., GROSS G., WIDERA G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN (2)
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN (3)
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 74253317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 RL POTTS J.T. JR.;
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL: X05722; G1839; -.
 DR PIR: A01535; PTPG.
 DR PIR: B26806; B26806.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPER 26 31
 FT CHAIN 32 115
 FT SEQUENCE 115 AA; 12852 MW; 98B67F47 CRC32;
 SQ

Query Match 100.0%; Score 43; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 3.67e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: Thu Jul 30 10:03:25 1998
 Job time : 7 secs.

WIRE (TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jul 30 10:03:43 1998; MasPar time 3.80 Seconds
Molecular output not generated. 77.626 Million cell updates/sec

Title: >US-08-817-547A-4
Description: (1-7) from US08817547A.pep
Perfect Score: 43
Sequence: 1 SVSEIQL 7

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs. 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_fodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 19.611; Variance 15.404; scale 1.273

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	41	95.3	896	9	055544	HYPOTHETICAL 100.3 KD	1.43e+00
2	39	90.7	105	10	063473	PARATHYROID HORMONE (F	5.71e+00
3	39	90.7	764	8	P93756	RECEPTOR-LIKE PROTEIN	5.71e+00
4	38	88.4	325	3	016546	C35A11.2 PROTEIN.	1.12e+01
5	38	88.4	459	1	013724	HYPOTHETICAL 51.4 KD P	1.12e+01
6	38	88.4	717	11	041942	HYPOTHETICAL 82.9 KD P	1.12e+01
7	38	88.4	958	8	040554	PMLA-35.	1.12e+01
8	37	86.0	287	12	090794	ALPHA-1 TYPE III COLLA	2.16e+01
9	37	86.0	691	10	035804	JANUS PROTEIN TYROSINE	2.16e+01
10	37	86.0	714	10	P70593	A-KINASE ANCHORING PRO	2.16e+01
11	37	86.0	930	9	053173	MGPS.	2.16e+01
12	37	86.0	1145	3	094906	DNA POLYMERASE GAMMA (2.16e+01
13	37	86.0	1810	3	018038	CODED FOR BY C. ELEGAN	2.16e+01
14	37	86.0	2089	2	014676	KIAA0170 PROTEIN.	2.16e+01
15	37	86.0	3456	11	P89201	POLYPROTEIN.	2.16e+01
16	36	83.7	101	3	015625	(FRAGMENT).	4.10e+01
17	36	83.7	189	3	019478	FL5B9.1.	4.10e+01
18	36	83.7	203	1	003201	HYPOTHETICAL 23.4 KD P	4.10e+01
19	36	83.7	356	9	031461	YBGE PROTEIN.	4.10e+01
20	36	83.7	366	9	044163	LIPOPROTEIN PRECURSOR.	4.10e+01

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	055544	95.3	896	9	055544	HYPOTHETICAL 100.3 KD	1.43e+00	1
2	053473	90.7	105	10	063473	PARATHYROID HORMONE (F	5.71e+00	2
3	053473	90.7	764	8	P93756	RECEPTOR-LIKE PROTEIN	5.71e+00	3
4	053473	90.7	325	3	016546	C35A11.2 PROTEIN.	1.12e+01	4
5	053473	90.7	459	1	013724	HYPOTHETICAL 51.4 KD P	1.12e+01	5
6	053473	90.7	717	11	041942	HYPOTHETICAL 82.9 KD P	1.12e+01	6
7	053473	90.7	958	8	040554	PMLA-35.	1.12e+01	7
8	053473	90.7	287	12	090794	ALPHA-1 TYPE III COLLA	2.16e+01	8
9	053473	90.7	691	10	035804	JANUS PROTEIN TYROSINE	2.16e+01	9
10	053473	90.7	714	10	P70593	A-KINASE ANCHORING PRO	2.16e+01	10
11	053473	90.7	930	9	053173	MGPS.	2.16e+01	11
12	053473	90.7	1145	3	094906	DNA POLYMERASE GAMMA (2.16e+01	12
13	053473	90.7	1810	3	018038	CODED FOR BY C. ELEGAN	2.16e+01	13
14	053473	90.7	2089	2	014676	KIAA0170 PROTEIN.	2.16e+01	14
15	053473	90.7	3456	11	P89201	POLYPROTEIN.	2.16e+01	15
16	053473	90.7	101	3	015625	(FRAGMENT).	4.10e+01	16
17	053473	90.7	189	3	019478	FL5B9.1.	4.10e+01	17
18	053473	90.7	203	1	003201	HYPOTHETICAL 23.4 KD P	4.10e+01	18
19	053473	90.7	356	9	031461	YBGE PROTEIN.	4.10e+01	19
20	053473	90.7	366	9	044163	LIPOPROTEIN PRECURSOR.	4.10e+01	20

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	055544	95.3	896	9	055544	HYPOTHETICAL 100.3 KD	1.43e+00	1
2	053473	90.7	105	10	063473	PARATHYROID HORMONE (F	5.71e+00	2
3	053473	90.7	764	8	P93756	RECEPTOR-LIKE PROTEIN	5.71e+00	3
4	053473	90.7	325	3	016546	C35A11.2 PROTEIN.	1.12e+01	4
5	053473	90.7	459	1	013724	HYPOTHETICAL 51.4 KD P	1.12e+01	5
6	053473	90.7	717	11	041942	HYPOTHETICAL 82.9 KD P	1.12e+01	6
7	053473	90.7	958	8	040554	PMLA-35.	1.12e+01	7
8	053473	90.7	287	12	090794	ALPHA-1 TYPE III COLLA	2.16e+01	8
9	053473	90.7	691	10	035804	JANUS PROTEIN TYROSINE	2.16e+01	9
10	053473	90.7	714	10	P70593	A-KINASE ANCHORING PRO	2.16e+01	10
11	053473	90.7	930	9	053173	MGPS.	2.16e+01	11
12	053473	90.7	1145	3	094906	DNA POLYMERASE GAMMA (2.16e+01	12
13	053473	90.7	1810	3	018038	CODED FOR BY C. ELEGAN	2.16e+01	13
14	053473	90.7	2089	2	014676	KIAA0170 PROTEIN.	2.16e+01	14
15	053473	90.7	3456	11	P89201	POLYPROTEIN.	2.16e+01	15
16	053473	90.7	101	3	015625	(FRAGMENT).	4.10e+01	16
17	053473	90.7	189	3	019478	FL5B9.1.	4.10e+01	17
18	053473	90.7	203	1	003201	HYPOTHETICAL 23.4 KD P	4.10e+01	18
19	053473	90.7	356	9	031461	YBGE PROTEIN.	4.10e+01	19
20	053473	90.7	366	9	044163	LIPOPROTEIN PRECURSOR.	4.10e+01	20

RC TISSUE-THYROID, AND PARATHYROID;
 RA SCHMEIZER H.J., GROSS G., MAYER H.;
 RL ADV. GENE TECHNOL. 21:228-229(1984).
 DR EMBL; M54875; G601933; -.
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;

Query Match 90.7%; Score 39; DB 10; Length 105;
 Best Local Similarity 71.4%; Pred. No. 5.71e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 22 AISEIOL 28
 : : : : :
 QY 1 SYSEIOL 7

Search completed: Thu Jul 30 10:04:16 1998
 Job time : 33 secs.

CC Removal on an iminobiotin column followed by chromatography on a
 CC fractogel and reverse phase HPLC.
 SQ Sequence 16 AA;

Query Match 100.0%; Score 35; DB 25; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.24e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 svselq 15
 |||||
 QY 1 SVSEIQ 6

RESULT 2

ID W21947 standard: Protein; 20 AA.

AC W21947;

DT 30-JAN-1998 (first entry)

DE Fusion protein comprising linker and PTH 1-37 (residues 1-7).
 Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin;
 fusion protein; recombinant production; thrombin.
 Synthetic.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..1

FT Peptide /note= "Met(13-139) streptavidin residue"

FT Peptide 2..13

FT Peptide /note= "linker cleavable by thrombin"

FT Peptide 14..20

FT Peptide /note= "parathyroid hormone 1-37 (residues 1-7)"

PN WO9718314-A1.

PD 22-MAY-1997.

PF 06-NOV-1996; E04850.

PR 16-NOV-1995; DE-042702.

PA (BOE) BOEHRINGER MANNHEIM GMBH.

PI Kopetzki E;

PI WPI; 97-289290/26.

DR N-PSDB: T73911.

DR N-PSDB: T73911.

PT Recombinant production of peptide(s) as fusions with streptavidin
 attached via cleavable linker - especially for utrotropin and
 parathyroid hormone production

PT Example 3; Fig 3; 37pp; German.

PS The DNA encoding the present sequence, a linker and residues 1-7 of
 the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage
 optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII

CC fragment of pSAM-CORE, which contains the Met(13-139) streptavidin
 (SA) sequence, to give pSA-THRO-PTH. pSA-THRO-PTH and the lacIq

CC repressor plasmid PUBS500 were used to transform E. coli K12 RM82.
 The transformants were grown, with IPTG induction, in medium

CC containing kanamycin and ampicillin. Cells were harvested, lysed
 and isolated inclusion bodies solubilised in guanidine

CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer.
 The solution was clarified and the supernatant concentrated and

CC purified on a column of immobilised iminobiotin. The purified
 material was incubated with thrombin and the PTH 1-37 fragment

CC released, recovered by SA fragment removal on an iminobiotin
 column followed by chromatography on a fractogel and reverse phase

CC HPLC.

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Search completed: Thu Jul 30 10:07:41 1998
 Job time : 15 secs.

WIDEOR (TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:06:50 1998; MasPar time 3.00 Seconds
Molecular output not generated. 73.160 Million cell updates/sec

Title: >US-08-817-547A-5
Description: (1-6) from US08817547A.pep
Perfect Score: 35
Sequence: 1 SVSEIQ 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plf56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 17.547; Variance 15.799; scale 1.111

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	35	100.0	34	5	1H7H cyclic parathyroid ho	2.66e+01
2	35	100.0	34	5	1ZWA parathyroid hormone (2.66e+01
3	35	100.0	37	5	1HPH parathyroid hormone f	2.66e+01
4	35	100.0	115	2	JC4202 parathyroid hormone -	2.66e+01
5	35	100.0	115	1	PTNU parathyroid hormone p	2.66e+01
6	35	100.0	115	1	PTPG parathyroid hormone p	2.66e+01
7	35	100.0	303	2	A64150 hypothetical protein	2.66e+01
8	35	100.0	853	2	S34682 probable transport pr	2.66e+01
9	35	100.0	1116	2	S41915 DNA-directed RNA poly	2.66e+01
10	33	94.3	37	5	1ZWC parathyroid hormone (8.67e+01
11	33	94.3	115	2	PTBO parathyroid hormone p	8.67e+01
12	33	94.3	115	2	A05091 parathyroid hormone p	8.67e+01
13	33	94.3	315	2	E69400 3-hydroxyacyl-CoA de	8.67e+01
14	33	94.3	424	2	I39310 zinc finger protein 1	8.67e+01
15	33	94.3	428	2	A43311 A-kinase anchor prote	8.67e+01
16	33	94.3	540	2	S35071 auxin-resistance prot	8.67e+01
17	33	94.3	801	2	PC6010 RNA helicase Gu - hum	8.67e+01
18	33	94.3	896	2	S59990 phycobilisome anchor	8.67e+01
19	33	94.3	896	2	S76064 hypothetical protein	8.67e+01
20	32	91.4	270	2	B32835 hypothetical ntra pro	1.53e+02
21	32	91.4	329	2	G69210 conserved hypothetical	1.53e+02
22	32	91.4	422	2	A34589 lin-10 protein - Cae	1.53e+02
23	32	91.4	507	2	B69957 conserved hypothetical	1.53e+02

24	32	91.4	537	2	S50344 aspergillopepsin homo	1.53e+02
25	32	91.4	697	2	G70133 flagellar biosynthet	1.53e+02
26	31	88.6	109	5	1VTG epsilon thrombin (EC	2.66e+02
27	31	88.6	109	5	1UCYE thrombin (EC 3.4.21.5	2.66e+02
28	31	88.6	146	2	S76533 hypothetical protein	2.66e+02
29	31	88.6	259	5	1TRBOH thrombin (EC 3.4.21.5	2.66e+02
30	31	88.6	259	5	1TRBK thrombin (EC 3.4.21.5	2.66e+02
31	31	88.6	259	5	1IBRK thrombin (EC 3.4.21.5	2.66e+02
32	31	88.6	259	5	1UCYK thrombin (EC 3.4.21.5	2.66e+02
33	31	88.6	259	5	1UCYK thrombin (EC 3.4.21.5	2.66e+02
34	31	88.6	259	5	1VTRH alpha thrombin (EC 3.	2.66e+02
35	31	88.6	259	5	1VTRH thrombin (EC 3.4.21.5	2.66e+02
36	31	88.6	298	2	S76437 hypothetical protein	2.66e+02
37	31	88.6	392	2	A69474 myo-inositol-1-phosph	2.66e+02
38	31	88.6	402	2	S47329 Oxa1 protein precursor	2.66e+02
39	31	88.6	415	2	S63221 DNA-directed RNA poly	2.66e+02
40	31	88.6	416	2	C47017 probable transcriptio	2.66e+02
41	31	88.6	635	2	S19011 endo-1,4-beta-xylanas	2.66e+02
42	31	88.6	677	2	S33664 flagella-associated p	2.66e+02
43	31	88.6	994	2	A47474 MADP-ADP-ribosyltrans	2.66e+02
44	31	88.6	1039	2	S02711 cellulase (EC 3.2.1.4	2.66e+02
45	31	88.6	3066	1	JQ1662 genome polyprotein -	2.66e+02

ALIGNMENTS

RESULT	1	1H7H	#type complete
ENTRY		cyclic parathyroid hormone residues 1-34 mutant M8NLE,	
TITLE		K130RN, S17E, M18NLE - synthetic	
PDB_TITLE		the solution structure of cyclic human parathyroid hormone	
ORGANISM		fragment 1 - 34, NMR, 10 structures	
REFERENCE		#formal_name synthetic	
authors		A68105	
#authors		Roesch, P.; Seidel, G.; Schaefer, W.; Esswein, A.; Hofmann,	
E.			
#submission		submitted to the Brookhaven Protein Data Bank, April 1997	
#cross-references		PDB:1H7H	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	
KEYWORDS		cyclic; human parathyroid hormone; nonleucine NMR structure;	
ornithine			
FEATURE			
4-6		#region helix (right hand 3-10) \	
20-29		#region helix (right hand alpha)	
SUMMARY		#length 34 #molecular-weight 4146 #checksum 5768	
Query Match		100.0%; Score 35; DB 5; Length 34;	
Best local Similarity 100.0%; Pred. No. 2.66e+01;			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	1	SVSEIQ 6	
Oy	1	SVSEIQ 6	
RESULT	2	1ZWA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		HPRH(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
authors		Roesch, P.; Marx, U.C.	
#authors		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:1ZWA	
REFERENCE		TN001717	
authors		Marx, U.C.	
#authors			
COMMENT		In Strukturen Verschiedener Parathormonfragmente in Loesung,	
COMMENT		pp.0, Bayreuth : Universitaet Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	

```

KEYWORDS          hormone
FEATURE
6-9               #region helix (right hand alpha)
19-30             #region helix (right hand alpha)
SUMMARY           #length 34 #molecular-weight 4118 #checksum 5629

Query Match       100.0%; Score 35; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.66e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SVSEIQ 6
OY 1 SVSEIQ 6
  
```

Search completed: Thu Jul 30 10:07:08 1998
 Job time : 18 secs.

MUSCLE

(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:05:44 1998; MasPar time 2.12 Seconds
Molecular output not generated. 70.907 Million cell updates/sec

Title: >US-08-817-547A-5
Description: (1-6) from US08817547A.pep
Perfect Score: 35
Sequence: 1 SVSEIO 6

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swlssl

Statistics: Mean 18.271; Variance 12.955; scale 1.410

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	35	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	5.84e+00
2	35	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	5.84e+00
3	35	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	5.84e+00
4	35	100.0	303	1	Y367_HAEIN HYPOTHETICAL PROTEIN H	5.84e+00
5	35	100.0	853	1	PXA2_YEAST PEROXISOMAL LONG-CHAIN	5.84e+00
6	35	100.0	1116	1	RPOB_HETCA DNA-DIRECTED RNA POLYM	5.84e+00
7	35	94.3	112	1	GLNB_MYCTU NITROGEN REGULATORY PR	2.41e+01
8	33	94.3	115	1	PTHY_RAT PARATHYROID HORMONE PR	2.41e+01
9	33	94.3	370	1	CPR3_CAEL CATHEPSIN B-LIKE CYSTE	2.41e+01
10	33	94.3	428	1	AK75_BOVIN A-KINASE ANCHOR PROTEI	2.41e+01
11	33	94.3	540	1	AKR1_ARATH AUXIN-RESISTANCE PROTE	2.41e+01
12	33	94.3	540	1	APCE_SYNY4 PHYCOBLITISOME 100.5 KD	2.41e+01
13	32	91.4	270	1	YHMG_RHIME PROBABLE ABC TRANSPORT	4.75e+01
14	32	91.4	417	1	LI10_CAEL LIN-10 PROTEIN.	4.75e+01
15	32	91.4	507	1	YOGP_BACSU PUTATIVE ASPARTYL PROT	4.75e+01
16	32	91.4	537	1	Y1V9_YEAST HYPOTHETICAL 56.4 KD P	4.75e+01
17	32	91.4	537	1	Y1V9_YEAST PUTATIVE ASPARTYL PROT	4.75e+01
18	31	88.6	164	1	Y646_METUA MEIOTIC RECOMBINATION	9.18e+01
19	31	88.6	180	1	RE15_SCHPO HYPOHETICAL PROTEIN M	9.18e+01
20	31	88.6	282	1	V174_CAEL VITELLOGENIN 4 PRECURS	9.18e+01
21	31	88.6	402	1	OXAI_YEAST CYTOCHROME OXIDASE BIO	9.18e+01
22	31	88.6	415	1	RPA3_YEAST DNA-DIRECTED RNA POLYM	9.18e+01
23	31	88.6	416	1	RPSC_AMASP RNA POLYMERASE SIGMA-C	9.18e+01

24	31	88.6	567	1	CYDC_BACSU TRANSPORT ATP-BINDING	9.18e+01
25	31	88.6	594	1	BAIK_DROME I KAPPA-RECOMBINATION	9.18e+01
26	31	88.6	602	1	VEL_HPV15 REPLICATION PROTEIN E1	9.18e+01
27	31	88.6	608	1	RDOF_SCEOB PROBABLE REVERSE TRANS	9.18e+01
28	31	88.6	625	1	THRB_BOVIN PROTHROMBIN PRECURSOR	9.18e+01
29	31	88.6	635	1	XYND_BACPO ENDO-1,4-BETA-XYLANASE	9.18e+01
30	31	88.6	677	1	FLHA_BACSU FLAGELLAR BIOSYNTHESIS	9.18e+01
31	31	88.6	727	1	CADA_STANU PROBABLE CADMIUM-TRANS	9.18e+01
32	31	88.6	804	1	CADD_STANU PROBABLE CADMIUM-TRANS	9.18e+01
33	31	88.6	937	1	ODOL_DROME 2-OXOGUTARATE DEHYDRO	9.18e+01
34	31	88.6	994	1	POL1_DROME POLY (ADP-RIBOSE) POLY	9.18e+01
35	31	88.6	1039	1	GUNB_CALSA ENOGLUCANASE B PRECUR	9.18e+01
36	31	88.6	1827	1	CUT1_SCHPO CUT1 PROTEIN.	9.18e+01
37	30	85.7	115	1	YSC1_YERN YOP PROTEINS TRANSLOCA	1.73e+02
38	30	85.7	275	1	FABH_ECOLI K88 MINOR FIMBRIAL SUB	1.73e+02
39	30	85.7	265	1	PORI_WHEAT OUTER MITOCHONDRIAL SUB	1.73e+02
40	30	85.7	342	1	YH22_YEAST HYPOTHETICAL 38.6 KD P	1.73e+02
41	30	85.7	381	1	PTX3_MOUSE PENTAXIN-RELATED PROTE	1.73e+02
42	30	85.7	982	1	Y596_CAEL HYPOTHETICAL 110.4 KD	1.73e+02
43	30	85.7	1131	1	YMS2_CAEL PUTATIVE ATP-DEPENDENT	1.73e+02
44	30	85.7	2329	1	Y589_CAEL HYPOTHETICAL 254.3 KD	1.73e+02
45	30	85.7	2412	1	POLI_BAYMG GENOME POLYPROTEIN 1 (1.73e+02

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	115 AA.
AC	PTHY_PIG			
AC	P01269;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	SUS SCROFA (PIG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUHAROTIA; ARTIODACTYLA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87316938.			
RA	SCHMELZER H.-J., GROSS G., WIDERA G., MAYER H.;			
RL	NUCLEIC ACIDS RES. 15:6740-6740(1987).			
RN	[2]			
RP	SEQUENCE OF 26-115.			
RX	MEDLINE; 76018954.			
RA	CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W., COHN D.V.;			
RL	BIOCHEMISTRY 14:3631-3635(1975).			
RN	[3]			
RP	SEQUENCE OF 32-115.			
RX	MEDLINE; 74253317.			
RA	SAVER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,			
RL	POUTS J.T., JR.;			
CC	BIOCHEMISTRY 13:1994-1999(1974).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL; X05722; GI839; .			
DR	PIR; A01535; PIRG.			
DR	PIR; B26806; B26806.			
DR	PROSITE; PS00335; PARATHYROID; 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL	1	25	
FT	PROPEP	26	31	
FT	CHAIN	32	115	
SQ	SEQUENCE	115 AA;	12852 MW;	98867F47 CRC32;
Query Match				
Best Local Similarity 100.0%; Score 35; DB 1; Length 115;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	32 SVSEIO 37			
Oy	1 SVSEIO 6			

```

RESULT 2
ID      PTH_CANFA      STANDARD:      PRT:      115 AA.
AC      P52212;
DT      01-OCT-1996 (REL. 34, CREATED)
DT      01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN      PTH.
OS      CANIS FAMILIARIS (DOG).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC      EUHERIA; CARNIVORA.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-PARATHYROID.
RX      MEDLINE: 95369696.
RA      ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
RA      DEMILLE J.W., CAPEN C.C.;
RA      GENE 160:241-243(1995).
        -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
        BONE AND PREVENTING THEIR RENAL EXCRETION.
DR      EMBL: U15662; G558916; -
DR      PROSITE: PS00335; PARATHYROID; 1.
KM      HORMONE; SIGNAL.
FT      SIGNAL. 1 25 BY SIMILARITY.
FT      PROPEP 26 31 BY SIMILARITY.
FT      CHAIN 32 115 PARATHYROID HORMONE.
SQ      SEQUENCE 115 AA; 12957 MW; 16ED0BEC CRC32;

Query Match      100.0%; Score 35; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.84e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB      32 SVSEIQ 37
QY      1 SVSEIQ 6

```

Search completed: Thu Jul 30 10:05:51 1998
Job time : 7 secs.

W O S E R H
(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:06:08 1998; Maspar time 3.81 Seconds
Abular output not generated. 66.309 Million cell updates/sec

Title: >US-08-817-547A-5
Description: (1-6) from US08817547A.pep
Perfect Score: 35
Sequence: 1 SVSEIQ 6

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 17.730; Variance 12.970; scale 1.367

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	35	100.0	714	10	P70593	A-KINASE ANCHORING PRO	8.71e+00
2	35	100.0	771	3	Q20026	CODED FOR BY C. ELEGAN	8.71e+00
3	33	94.3	315	9	Q29062	3-HYDROXYACYL-COA DEH	3.59e+01
4	33	94.3	324	9	O07213	HYPOHETICAL 35.5 KD P	3.59e+01
5	33	94.3	424	2	Q15916	ZID, ZINC FINGER PROTE	3.59e+01
6	33	94.3	484	2	O18032	TOSF1A.4.	3.59e+01
7	33	94.3	794	4	O18742	LU-ECAM-1.	3.59e+01
8	33	94.3	801	2	O13436	NUCLEOLAR RNA HELICASE	3.59e+01
9	33	94.3	820	4	O18743	LU-ECAM-1.	3.59e+01
10	33	94.3	896	9	O55544	HYPOHETICAL 100.3 KD	3.59e+01
11	33	94.3	905	4	O18741	LU-ECAM-1.	3.59e+01
12	33	94.3	1967	11	O10378	LARGE PROTEIN.	3.59e+01
13	32	91.4	43	2	O14359	GALACTOSE-1-PHOSPHATE	7.10e+01
14	32	91.4	91	9	P72152	FLAG.	7.10e+01
15	32	91.4	131	11	P87572	E4 ORF1.	7.10e+01
16	32	91.4	239	9	P74971	PV. VESICATORIA ORF1.	7.10e+01
17	32	91.4	258	9	O52785	ABC-TYPE PERMEASE HOMO	7.10e+01
18	32	91.4	270	9	O53342	ORE 5' OF RION.	7.10e+01
19	32	91.4	317	11	O66606	VIRAL NUCLEOPROTEIN.	7.10e+01
20	32	91.4	329	9	O26918	CONSERVED PROTEIN.	7.10e+01

21	32	91.4	466	2	O13283	GAP SH3 BINDING PROTEI	7.10e+01
22	32	91.4	595	1	O14301	BETA-TRANSUDOCIN.	7.10e+01
23	32	91.4	673	9	O44759	FLHA.	7.10e+01
24	32	91.4	679	8	O39603	HEAT SHOCK PROTEIN 70B	7.10e+01
25	32	91.4	697	9	O44909	FLAGELLAR EXPORT PROTE	7.10e+01
26	31	88.6	105	10	O63473	PARATHYROID HORMONE (F	1.37e+02
27	31	88.6	146	9	O53737	HYPOHETICAL 16.4 KD P	1.37e+02
28	31	88.6	251	3	O26980	ZEN TC (FRAGMENT).	1.37e+02
29	31	88.6	265	9	O07802	HYPOHETICAL 27.4 KD P	1.37e+02
30	31	88.6	292	2	O14538	MACROPHAGE LECTIN 2.	1.37e+02
31	31	88.6	298	9	P74465	PLIN BIOGENESIS PROTE	1.37e+02
32	31	88.6	311	9	P71859	HYPOHETICAL 33.9 KD P	1.37e+02
33	31	88.6	316	9	O47701	POLYSACCHARIDE CHAIN L	1.37e+02
34	31	88.6	444	9	O51919	PUTATIVE CHAPERONIN (1.37e+02
35	31	88.6	465	10	P97855	RAS-GTPASE-ACTIVATING	1.37e+02
36	31	88.6	471	4	P79386	ORPHAN NUCLEAR RECEPT	1.37e+02
37	31	88.6	625	10	O61468	MEGARACOCYTE POTENTIA	1.37e+02
38	31	88.6	764	8	P93756	RECEPTOR-LIKE PROTEIN	1.37e+02
39	31	88.6	815	8	O22113	HCR2.	1.37e+02
40	31	88.6	939	1	O06078	SIMILAR TO TRANSCRIPTI	1.37e+02
41	31	88.6	1026	11	O36363	DNA POLYMERASE (EC 2.7	1.37e+02
42	31	88.6	1106	2	O15034	KIA0318 (FRAGMENT).	1.37e+02
43	31	88.6	1144	3	P91304	CODED FOR BY C. ELEGAN	1.37e+02
44	31	88.6	1277	12	O98902	NEURAL CELL ADHESION M	1.37e+02
45	31	88.6	1819	3	O16625	K1066.3 PROTEIN.	1.37e+02

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	714 AA.
AC	P70593			
DT	01-FEB-1997 (TREMBLREL. 02, CREATED)			
DT	01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)			
DT	01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)			
DE	A-KINASE ANCHORING PROTEIN AKAP150.			
OS	RATTUS NORVEGICUS (RAT)			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	TAKAI Y., IRIE M., TOYODA A., HATA Y.;			
RL	SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL: U67136; G1532182; .			
SO	SEQUENCE 714 AA; 75938 MW; 0A1CFCLF CRC32;			

Query Match 100.0%; Score 35; DB 10; Length 714;
Best Local Similarity 100.0%; Pred. No. 8.71e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	4 SVSEIQ 9	1 SVSEIQ 6
QY		
RESULT	2	
AC	Q20026;	PRELIMINARY: PRT; 771 AA.
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)	
DE	CODED FOR BY C. ELEGANS	
GN	F5C8.7.	
OS	CAENORHABDITIS ELEGANS.	
OC	EUKARYOTA; METAZOA; ACLOMATES; NEMATODA; SECCERENTEA; RHABDITIDA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE: 94150718.	
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,	
RA	BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,	
RA	CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,	
RA	GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSON L.,	
RA	JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,	

RA LIGHTNING J., LLOYD C., MCGRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RL NATURE 368:32-38(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RA WD X;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WATERSTON R.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U40941; G1072187; -;
 SQ SEQUENCE 771 AA; 87311 MW; 5AE2EE3F CRC32;

Query Match 100.0%; Score 35; DB 3; Length 771;
 Best Local Similarity 100.0%; Pred. No. 8.71e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 190 SYSEIO 195
 |||||
 QY 1 SYSEIO 6

Search completed: Thu Jul 30 10:06:33 1998
 Job time : 25 secs.

CC removal on an iminobiotin column followed by chromatography on a
 CC fractogel and reverse phase HPLC.
 SQ Sequence 16 AA;

Query Match 100.0%; Score 28; DB 25; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.96e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 svsel 14
 |||||
 QY 1 SVSEI 5

RESULT 2
 ID W21947 standard; Protein; 20 AA.
 AC W21947;
 DT 30-JAN-1998 (first entry)
 DE Fusion protein comprising linker and PTH 1-37 (residues 1-7).
 Linker: parathyroid hormone 1-37; PTH 1-37; streptavidin;
 fusion protein; recombinant production; thrombin.
 US Synthetic.
 FH Homo sapiens.
 Key Location/Qualifiers
 FT Peptide 1..1
 FT /note= "Met(13-139) streptavidin residue"
 FT Peptide 2..13
 FT /note= "Linker cleavable by thrombin"
 FT Peptide 14..20
 FT /note= "parathyroid hormone 1-37 (residues 1-7)"
 PN W09718314-A1.
 PD 22-MAY-1997.
 PF 06-NOV-1996; E04850.
 PR 16-NOV-1995; DE-042702.
 PA (BOEP) BOEHRINGER MANNHEIM GMBH.
 PI Kopeckzi E;
 DR WPI: 97-289290/26.
 DR N-PSDB; T73911.
 DT Recombinant production of peptide(s) as fusions with streptavidin
 PT attached via cleavable linker - especially for urotropin and
 PT parathyroid hormone production
 PT parathyroid hormone production
 PS Example 3: Fig 3; 37pp; German.
 CC The DNA encoding the present sequence, a linker and residues 1-7 of
 CC the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage
 CC optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII
 CC fragment of PSAM-CORE, which contains the Met(13-139) streptavidin
 CC (SA) sequence, to give PSA-THRO-PTH. PSA-THRO-PTH and the lacIq
 CC repressor plasmid pUBS500 were used to transform E. coli K12 RM82.
 CC The transformants were grown, with IPTG induction, in medium
 CC containing kanamycin and ampicillin. Cells were harvested, lysed
 CC and isolated inclusion bodies solubilised in guanidine
 CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer.
 CC The solution was clarified and the supernatant concentrated and
 CC purified on a column of immobilised iminobiotin. The purified
 CC material was incubated with thrombin and the PTH 1-37 fragment
 CC released recovered by SA fragment removal on an iminobiotin
 CC column followed by chromatography on a fractogel and reverse phase
 CC HPLC.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 28; DB 25; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.96e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 14 svsel 18
 |||||
 QY 1 SVSEI 5

Search completed: Thu Jul 30 10:09:58 1998
 Job time : 16 secs.

KEYWORDS hormone
FEATURE 6-9 #region helix (right hand alpha) \
19-30 #region helix (right hand alpha) \
SUMMARY #length 34 #molecular-weight 418 #checksum 5629
Query Match 100.0%; Score 28; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.60e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 SVSEI 5
QY 1 SVSEI 5

Search completed: Thu Jul 30 10:09:24 1998
Job time : 18 secs.

WIDEORIT (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:07:59 1998; MasPar time 2.00 Seconds
Tabular output not generated. 62.621 Million cell updates/sec

Title: >US-08-817-547A-6
Description: (1-5) from US08817547A.pep
Perfect Score: 28
Sequence: 1 SVSEI 5

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 16.927; Variance 10.693; scale 1.583

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	28	100.0	93	1 TRBJ_ECOLI	TUBULIN PROTEIN.	1.27e+02
2	28	100.0	115	1 PTHY_CANFA	PARATHYROID HORMONE PR	1.27e+02
3	28	100.0	115	1 PTHY_HUMAN	PARATHYROID HORMONE PR	1.27e+02
4	28	100.0	115	1 PTHY_PIG	PARATHYROID HORMONE PR	1.27e+02
5	28	100.0	197	1 TBA_PLAJO	TUBULIN ALPHA CHAIN (F	1.27e+02
6	28	100.0	212	1 TBA_PNECA	TUBULIN ALPHA CHAIN (F	1.27e+02
7	28	100.0	227	1 YMYO_YEAST	HYPOTHETICAL 24.9 KD P	1.27e+02
8	28	100.0	303	1 Y367_HAEIN	HYPOTHETICAL PROTEIN H	1.27e+02
9	28	100.0	316	1 TALB_ECOLI	TRANSALDOLASE B (EC 2.	1.27e+02
10	28	100.0	324	1 TBA8_CHICK	TUBULIN ALPHA-8 CHAIN	1.27e+02
11	28	100.0	362	1 PG12_ASPNG	POLYGALACTURONASE II P	1.27e+02
12	28	100.0	362	1 PG12_ASPFU	POLYGALACTURONASE II P	1.27e+02
13	28	100.0	389	1 CHS3_TRISU	CHALCONE SYNTHASE 3 (E	1.27e+02
14	28	100.0	389	1 CHS4_MEDSA	CHALCONE SYNTHASE 4 (E	1.27e+02
15	28	100.0	389	1 CHS5_MEDSA	CHALCONE SYNTHASE 4-2	1.27e+02
16	28	100.0	389	1 CHS3_MEDSA	CHALCONE SYNTHASE 4-1	1.27e+02
17	28	100.0	389	1 CHS1_PLAVU	CHALCONE SYNTHASE 17 (1.27e+02
18	28	100.0	389	1 CHS1_PEA	CHALCONE SYNTHASE 1 (E	1.27e+02
19	28	100.0	389	1 CHS3_PEA	CHALCONE SYNTHASE 3 (E	1.27e+02
20	28	100.0	389	1 CHS8_MEDSA	CHALCONE SYNTHASE 8 (E	1.27e+02
21	28	100.0	389	1 CHS9_MEDSA	CHALCONE SYNTHASE 9 (E	1.27e+02
22	28	100.0	404	1 FRHA_METTH	COENZYME F420 HYDROGEN	1.27e+02
23	28	100.0	415	1 RPA3_YEAST	DNA-DIRECTED RNA POLYM	1.27e+02

24	28	100.0	445	1 TBA3_YEAST	TUBULIN ALPHA-3 CHAIN.	1.27e+02
25	28	100.0	447	1 TBA1_YEAST	TUBULIN ALPHA-1 CHAIN.	1.27e+02
26	28	100.0	448	1 TBA_CANAL	TUBULIN ALPHA CHAIN.	1.27e+02
27	28	100.0	451	1 TBA_TORMA	TUBULIN ALPHA CHAIN (A	1.27e+02
28	28	100.0	451	1 TBA_TRYBR	TUBULIN ALPHA CHAIN.	1.27e+02
29	28	100.0	453	1 TBA_PLAFC	TUBULIN ALPHA CHAIN.	1.27e+02
30	28	100.0	458	1 YKH3_CAEEL	HYPOTHETICAL ACETYLCHO	1.27e+02
31	28	100.0	493	1 PUR1_SYNP7	AMIDOPHOSPHORIBOSYLTRA	1.27e+02
32	28	100.0	609	1 YL01_YEAST	HYPOTHETICAL 69.8 KD P	1.27e+02
33	28	100.0	609	1 DNAK_MYCDE	DNAK PROTEIN.	1.27e+02
34	28	100.0	621	1 DNAK_MYCDE	DNAK PROTEIN (HEAT SHO	1.27e+02
35	28	100.0	644	1 KXH_HUMAN	KININOGEN_HMW PRECURS	1.27e+02
36	28	100.0	737	1 SUV3_YEAST	MITOCHONDRIAL ATP-DEPE	1.27e+02
37	28	100.0	921	1 SECA_CAUCR	PREPROTEIN TRANSLOCASE	1.27e+02
38	28	100.0	962	1 Y4AE_SCHPO	HYPOTHETICAL TRP-ASP R	1.27e+02
39	28	100.0	974	1 SIN4_YEAST	GLOBAL TRANSCRIPTIONAL	1.27e+02
40	28	100.0	1039	1 GUNB_CALSA	ENOGLUCANASE B PRECUR	1.27e+02
41	28	100.0	1116	1 KROB_HERCA	DNA-DIRECTED RNA POLYM	1.27e+02
42	28	100.0	1146	1 KTXA_KLUFA	KILDER TOXIN ALPHA AND	1.27e+02
43	28	100.0	1332	1 CDP_MOUSE	CCAAT DISPLACEMENT PRO	1.27e+02
44	28	100.0	1505	1 CDP_HUMAN	CCAAT DISPLACEMENT PRO	1.27e+02
45	28	100.0	2916	1 YN81_CAEEL	HYPOTHETICAL 316.1 KD	1.27e+02

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	93 AA.
ID	TRBJ_ECOLI			
AC	PI8353;			
DT	01-NOV-1990 (REL. 16, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	TRBJ PROTEIN.			
GN	TRBJ.			
OS	ESCHERICHIA COLI.			
OC	PLASMID F.			
CC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS.			
OC	ENTEROBACTERIACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-K12;			
RX	MEDLINE; 89123020.			
RA	WU J.H., TEPPEL-THEER K.;			
RL	J. BACTERIOL. 171:213-221(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94359430.			
RA	FROST L.S., TEPPEL-THEER K., SKURRAY R.A.;			
RL	MICROBIOL. REV. 58:162-210(1994).			
CC	-1- FUNCTION: UNKNOWN.			
DR	EMBL; M20787; -; NOT_ANNOTATED_CDS.			
DR	EMBL; U01159; G398536; -.			
DR	PIR; F32238; Q0EC25.			
KW	PLASMID.			
SO	SEQUENCE 93 AA; 10160 MW; C604F894 CRC32;			
Query Match 100.0%; Score 28; DB 1; Length 93;				
Best Local Similarity 100.0%; Pred. No. 1.27e+02;				
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
DB	66 SVSEI 70			
QY	1 SVSEI 5			
RESULT 2				
ID	PTHY_CANFA	STANDARD;	PRT;	115 AA.
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			

OS CANIS FAMILIARIS (DOG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; CARNIVORA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-PARATHYROID;
 RX MEDLINE: 95369696.
 RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
 RL DEWILLE J.W., CAPEN C.C.;
 CC GENE 160:241-243(1995).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 DR BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL: U15662; G558916; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SO SEQUENCE 115 AA; 12957 MW; 16D0DEBC CRC32;
 Query Match 100.0%; Score 28; DB 1; Length 115;
 Best Local Similarity 100.0%;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 SVSET 36
 QY 1 SVSET 5

Search completed: Thu Jul 30 10:08:06 1998
 Job time : 7 secs.

M P E R E L I
(TM)

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MPsrch_p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:08:23 1998; MapPar time 3.56 Seconds
59.081 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-6
Description: (1-5) from US08817547A.pep
Perfect Score: 28
Sequence: 1 SVSET 5

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_protein 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 16.468; Variance 10.714; scale 1.537

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	28	100.0	82	9	030721	HYPOTHETICAL 9.0 KD PR	1.95e+02
2	28	100.0	110	3	016290	F32D1.8 PROTEIN.	1.95e+02
3	28	100.0	113	9	051810	HYPOTHETICAL 12.6 KD P	1.95e+02
4	28	100.0	126	9	P95985	ORF C04047.	1.95e+02
5	28	100.0	189	3	Q19478	F15B9.1.	1.95e+02
6	28	100.0	228	2	Q15631	TRANSLIN.	1.95e+02
7	28	100.0	228	10	P97891	TRANSLIN.	1.95e+02
8	28	100.0	228	10	062348	TRANSLIN.	1.95e+02
9	28	100.0	260	3	Q15744	PKSB.	1.95e+02
10	28	100.0	291	9	Q28438	METHIONYL AMINOPEPTIDA	1.95e+02
11	28	100.0	338	9	Q44791	ERPD.	1.95e+02
12	28	100.0	350	9	Q47506	PLASMOD PMSCC7 MCCA.B,	1.95e+02
13	28	100.0	377	3	P92126	ALPHA-TUBULIN (FRAGMENT	1.95e+02
14	28	100.0	378	9	Q31328	ERRV.	1.95e+02
15	28	100.0	389	8	Q23884	CHALCONE SYNTHASE (EC	1.95e+02
16	28	100.0	389	8	Q23882	CHALCONE SYNTHASE (EC	1.95e+02
17	28	100.0	389	8	Q23883	CHALCONE SYNTHASE (EC	1.95e+02
18	28	100.0	394	8	Q43809	1-AMINOCYCLOPROPANE 1-	1.95e+02
19	28	100.0	420	9	Q25039	EXONUCLEASE VII, LARGE	1.95e+02
20	28	100.0	425	3	Q26973	ALPHA-TUBULIN.	1.95e+02

RESULT	ID	PRELIMINARY	PRT	82 AA.	ALIGNMENTS
1	030721				
AC	030721				
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DE	HYPOTHETICAL 9.0 KD PROTEIN (FRAGMENT).				
OS	HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).				
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA.				
NC	AEROBIC, MOTILE, HELICAL AND/OR VIRIOTID.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CCUG 17874;				
RA	MASIGNANT V., ARICO' B.;				
RL	SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
DR	EMBL; AF016039; G267603; --				
KW	HYPOTHETICAL PROTEIN.				
FT	NON_TER 82				
SO	SEQUENCE 82 AA; 9025 MW; 25304A67 CRC32;				
Query Match	100.0%; Score 28; DB 9; Length 82;				
Best Local Similarity	100.0%; Pred. No. 1.95e+02;				
Matches	5; Conservative				
Mismatches	0; Indels 0; Gaps 0;				

Db	6 SVSET 10	PRELIMINARY	PRT	110 AA.
QY	1 SVSET 5			
RESULT	2			
ID	016290			
AC	016290			
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DE	F32D1.8 PROTEIN.			
GN	F32D1.8.			
OS	CAENORHABDITIS ELEGANS.			
NC	EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.			
RC	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RX	MEDLINE: 94150718.			
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,			

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STILSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ.
RA BECKER M., BRADSHAW H., KRAMER J.,
RL SUBMITTED (Aug-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ.
RA WATERSTON R.,
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL, AF016427; G2291235; -.
SEQUENCE 110 AA; 13038 MW; 9E338B0B CRC32;

Query Match 100.0%; Score 28; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.95e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 36 SVSEI 40
QY 1 SVSEI 5

Search completed: Thu Jul 30 10:08:48 1998
Job time : 25 secs.

Db 3 hnlqkhlmsm 12
 |||||
 QY 1 HNLGKHLNSM 10

RESULT 2

ID R74521 standard; Peptide; 34 AA.
 AC R74521;
 DT 04-DEC-1995 (first entry)
 DE Human parathyroid hormone (1-34).
 KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
 KW osteoporosis; hypercalcaemia; hyperparathyroidism;
 KW metabolic bone disease; human; veterinary medicine;
 KW iontophoretic transdermal transport; recombinant E.coli.
 OS Homo sapiens.
 PN W09511988-A.
 PD 04-MAY-1995
 PE 25-OCT-1994;
 PF 25-OCT-1993; US-142551.
 (AFY-) AFFYMAX TECHNOLOGIES NV.
 Oldenburg KR, Selick HE;
 WPI; 95-178880/23.
 DR New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 PS Disclosure; Page 1; 109pp; English.
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (hPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see R74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathyroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport compared to wild type
 CC PTH and can be produced in high yield in recombinant E.coli.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 73; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.59e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlqkhlmsm 18
 |||||
 QY 1 HNLGKHLNSM 10

Search completed: Thu Jul 30 10:12:36 1998
 Job time : 22 secs.

COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS hormone
FEATURE
15-25 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 73; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.13e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Db 6 HNLGKHLNSM 15
|||||
QY 1 HNLGKHLNSM 10

Search completed: Thu Jul 30 10:11:56 1998
Job time : 34 secs.

WATERMAN (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:10:15 1998; MasPar time 2.14 Seconds
117.135 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-7
Description: (1-10) from US08817547A.pep
Perfect Score: 73
Sequence: 1 HNLGKHLNSW 10

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.362; Variance 25.262; scale 0.925

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	73	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.53e-06
2	69	94.5	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.99e-05
3	63	94.5	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.99e-05
4	62	84.9	115	1	PTHY_PIG PARATHYROID HORMONE PR	1.50e-03
5	59	80.8	115	1	PTHY_RAT PARATHYROID HORMONE PR	8.86e-03
6	48	65.8	171	1	PAIA_BACSU PROTEASE SYNTHASE AND	3.78e+00
7	48	65.8	381	1	DHB2_MOUSE ESTRADIOL 17 BETA-DEHY	3.78e+00
8	48	65.8	887	1	MTS4_SCHPO 26S PROTEASOME REGULAT	3.78e+00
9	47	64.4	187	1	ATPD_ODOSI ATP SYNTHASE DELTA CHA	6.28e+00
10	47	64.4	621	1	PLAK_MOUSE JUNCTION PLAKOGLOBIN (6.28e+00
11	47	64.4	738	1	PLAK_XENLA JUNCTION PLAKOGLOBIN (6.28e+00
12	47	64.4	743	1	PLAK_HUMAN JUNCTION PLAKOGLOBIN (6.28e+00
13	46	63.0	152	1	HMGH_SOYBN HMG-Y RELATED PROTEIN	1.03e+01
14	46	63.0	176	1	HMGH_SOYBN HMG-Y RELATED PROTEIN	1.03e+01
15	46	63.0	192	1	SC72_YEAST TRANSLOCATION PROTEIN	1.03e+01
16	46	63.0	417	1	HS47_RAT 47 KD HEAT SHOCK PROTE	1.03e+01
17	46	63.0	417	1	HS47_HUMAN 47 KD HEAT SHOCK PROTE	1.03e+01
18	46	63.0	417	1	HS47_MOUSE 47 KD HEAT SHOCK PROTE	1.03e+01
19	46	63.0	418	1	CBP2_HUMAN COLLAGEN-BINDING PROTE	1.03e+01
20	46	63.0	2068	1	CCG1_DOMO TRANSCRIPTION INITIAT	1.03e+01
21	45	61.6	208	1	YFJ1_ECOLI HYPOTHERMAL 24.6 KD P	1.69e+01
22	45	61.6	405	1	HS47_CHICK 47 KD HEAT SHOCK PROTE	1.69e+01
23	45	61.6	700	1	PTPE_HUMAN PROTEIN-TYROSINE PHOSP	1.69e+01

RESULT	ID	PTHY_HUMAN	STANDARD	PRT	115 AA.	ALIGNMENTS
AC	21-JUL-1986	(REL. 01, CREATED)				
DT	13-AUG-1987	(REL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 82150870.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T., JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.,					
RL	HENDY G.N., POTTS J.T., JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RX	MEDLINE: 74174967.					
RA	JACOBS J.W., KEMPER B., NIML H.D., HABENER J.F., POTTS J.T., JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RX	MEDLINE: 7411656.					
RA	NIML H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,					
RL	O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T., JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RX	MEDLINE: 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,					
RL	POTTS J.T., JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NIML H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,					
RL	O'RIORDAN J.L.H., POTTS J.T., JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.,					
RL	PARSONS J.A., EDS., PP. 9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

RP REVIEWS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGGAR G.W., VAN RIESCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RX SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDREATTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA RINIER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345518.
 RA BARDEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MARX U.C., AUSTERMANN S., BAYER P., ADERMAN K., EICHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ANNOUD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 DR EMBL: J00301: G190704: -;
 DR EMBL: V00597: G37144: -;
 DR EMBL: A29146: E186700: -;
 DR PIR: A01536: PTHU.
 DR PIR: A19339: A19339.
 DR PDB: 1HPH: 10-JUL-95.
 DR PDB: 1HTH: 15-OCT-97.
 DR PDB: 12MB: 12-MAR-97.
 DR PDB: 12WC: 12-MAR-97.
 DR PDB: 12WD: 12-MAR-97.
 DR PDB: 12WE: 12-MAR-97.
 DR PDB: 12WF: 16-JUN-97.
 DR PDB: 12WG: 16-JUN-97.
 DR MTM: 146200: -;
 DR MTM: 168450: -;
 DR PROSITE: PS00335: PARATHYROID; 1.
 DR KWM: HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107 PARATHYROID HORMONE.
 FT SEQUENCE 115 AA: 12861 MM: 243B87C7 CRC32: C -> R (IN FTH; LEADS TO INEFFICIENT
 N -> D (IN REF. 5).
 Query Match 100.0%; Score 73; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1,53e-06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 HNLGKHLNSM 49
 QY 1 HNLGKHLNSM 10
 RESULT 2
 ID PTHY BOVIN STANDARD: PRT: 115 AA.
 AC P01268;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 80056617.
 RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
 RA POTTS J.T. JR., RICH A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 82037785.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 83105964.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84262483.
 RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
 RL GENE 28:319-329(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 74142666.
 RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
 RA COHN D.V.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
 RN [6]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 71076162.
 RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
 RA AURBACH G.D., POTTS J.T. JR.;
 RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
 RN [7]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 71063634.
 RA BREWER H.B. JR., ROMAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 71091588.
 RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
 RA DEFLOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL: V00106: G85: -;
 DR EMBL: J00023: G163641: -;
 DR EMBL: J00024: G163643: -;
 DR EMBL: J00024: E18249: ALT_SEQ.
 DR EMBL: J00024: E18250: ALT_SEQ.
 DR EMBL: K01938: G163647: -;
 DR EMBL: M25082: G163645: -;
 DR PIR: A01534: PTHO.
 DR PIR: A01534: PTHO.
 DR PROSITE: PS00335: PARATHYROID; 1.
 DR KWM: HORMONE; SIGNAL.

Thu Jul 30 13:38:21 1998

FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106
SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;
PARATHYROID HORMONE.
V -> G (IN REF. 4).

Query Match 94.5%; Score 69; DB 1; Length 115;
Best Local Similarity 90.0%; Pred. No. 1.99e-05;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKRLSSM 49
|||||:11
QY 1 HNLGKRLNSM 10

Search completed: Thu Jul 30 10:10:23 1998
Job time : 8 secs.



RL MOL. CELL. BIOL. 6:411-424(1986).
 DR EMBL: M13100; G804811; .
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;

Query Match 68.5%; Score 50; DB 10; Length 367;
 Best Local Similarity 66.7%;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 74 KLGKHLHW 82
 :|||||:
 QY 2 NLGKHLNSM 10

Search completed: Thu Jul 30 10:11:05 1998
 Job time : 24 secs.

WIRE (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:14:54 1998; MasPar time 2.63 Seconds
52.587 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-8
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 NLGKHLNSM 9

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.754; Variance 55.237; scale 0.285

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	64	100.0	34	22	W17957	Human parathyroid hor	3.96e+00
2	64	100.0	34	22	W17954	Human parathyroid hor	3.96e+00
3	64	100.0	34	22	W17968	Human parathyroid hor	3.96e+00
4	64	100.0	34	22	W17950	Human PTH analogue [C	3.96e+00
5	64	100.0	34	22	W17969	Human parathyroid hor	3.96e+00
6	64	100.0	34	22	W17951	Human parathyroid hor	3.96e+00
7	64	100.0	34	8	R41557	[Gln25,26,27]hPTH (1-	3.96e+00
8	64	100.0	34	8	R41550	[D-Ala3]hPTH (1-34).	3.96e+00
9	64	100.0	34	19	R98951	Target peptide (PTH(1	3.96e+00
10	64	100.0	34	22	W17955	Human parathyroid hor	3.96e+00
11	64	100.0	34	22	W17947	Human parathyroid hor	3.96e+00
12	64	100.0	34	22	W20000	Cyclised human parath	3.96e+00
13	64	100.0	36	9	R58272	[D-Lys13]-hPTH(1-36)-	3.96e+00
14	64	100.0	36	9	R58219	[Met26]-hPTH(1-36)-NH	3.96e+00
15	64	100.0	36	9	R58263	[D-Ile5]-hPTH(1-36)-N	3.96e+00
16	64	100.0	36	9	R58268	[Cha8]-hPTH(1-36)-NH2	3.96e+00
17	64	100.0	36	9	R58243	Propargy1-[Al1]-hPTH(1	3.96e+00
18	64	100.0	36	9	R58229	[Ala30]-hPTH(1-36)-NH	3.96e+00
19	64	100.0	36	9	R58290	[Ala26]-hPTH(1-36)-NH	3.96e+00

20	64	100.0	36	9	R58295	[D-Val35]-hPTH(1-36)-	3.96e+00
21	64	100.0	36	9	R58253	[4-aminobenzoic acid1	3.96e+00
22	64	100.0	36	9	R58252	[Asn1]-hPTH(1-36)-NH2	3.96e+00
23	64	100.0	37	9	R58244	[Ala0]-hPTH(1-36)-NH2	3.96e+00
24	64	100.0	38	9	R58148	[Ala22]-hPTH(1-38)-OH	3.96e+00
25	64	100.0	38	9	R58145	[Gly22]-hPTH(1-38)-OH	3.96e+00
26	64	100.0	38	9	R58125	[Leu19]-hPTH(1-38)-OH	3.96e+00
27	64	100.0	38	9	R58134	[Ile19]-hPTH(1-38)-OH	3.96e+00
28	64	100.0	38	9	R58269	[Leu8]-hPTH(1-38)-NH2	3.96e+00
29	64	100.0	38	9	R58024	[Ala1,Ile2]-hPTH(1-38	3.96e+00
30	64	100.0	38	19	R98958	Target peptide (PTH(1	3.96e+00
31	64	100.0	44	26	P30015	Human parathyroid hor	3.96e+00
32	64	100.0	47	25	W21945	Fusion protein complr	3.96e+00
33	64	100.0	84	27	W25687	Human parathyroid hor	3.96e+00
34	64	100.0	84	4	R21180	Human parathyroid hor	3.96e+00
35	64	100.0	84	4	R21181	Human parathyroid hor	3.96e+00
36	64	100.0	84	4	R21220	Human parathyroid hor	3.96e+00
37	64	100.0	84	4	R21194	Human parathyroid hor	3.96e+00
38	64	100.0	84	8	R42074	Stability-enhanced hu	3.96e+00
39	64	100.0	84	8	R42068	Stability-enhanced hu	3.96e+00
40	64	100.0	84	25	W29420	Human parathyroid hor	3.96e+00
41	64	100.0	84	4	R21175	Human parathyroid hor	3.96e+00
42	64	100.0	84	4	R21174	Human parathyroid hor	3.96e+00
43	64	100.0	84	4	R21231	Human parathyroid hor	3.96e+00
44	64	100.0	84	4	R21202	Human parathyroid hor	3.96e+00
45	64	100.0	84	4	R21158	Human parathyroid hor	3.96e+00

ALIGNMENTS

RESULT 1
ID W17957 standard; peptide: 34 AA.

AC W17957;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Alb3]hPTH(1-34)NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.

OS Homo sapiens.
OS Synthetic.

FT Key Location/Qualifiers
FT modified_site 3 /label= Alb

FT modified_site 34 /note= "in amide form"

FT W09702834-Al.

PD 30-JAN-1997.

PR 03-JUL-1996; U11292.

PR 13-JUL-1995; US-001105.

PR 06-SEP-1995; US-003305.

PR 29-MAR-1996; US-626186.

PA (BIOM-) BIOMEASURE INC.

PI Dong 2X;

DR WPI; 97-11819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which
stimulate bone growth and are used for treatment of osteoporosis and

PT bone fracture

PS Claim 11; Page -: 33p; English.

CC The present sequence is a specific example of a human parathyroid

CC hormone (hPTH) analogue from fragment 1-34 in which at least one

CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34

CC is alpha-aminoisobutyric acid (Aib). In this example the Ser residue

CC at position 3 of the wild-type has been substituted by Aib. The hPTH

CC analogues stimulate bone growth and so are useful in human or veterinary

CC medicine for treatment of osteoporosis and bone fracture, optionally in

CC conjunction with anti-resorptive therapy (bisphosphonates and

CC calcitonin).

CC N.B. The present sequence does not appear in the specification. It

CC corresponds to the known hPTH 1-34 fragment with the modifications

CC as stated in the claim.

CC Sequence 34 AA;

Query Match 100.0%; Score 64; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.96e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 nlghlnsm 18

QY 1 NLGRHLNSM 9

RESULT 2

ID M17954 standard; peptide; 34 AA.

AC M17954; 29-JUL-1997 (first entry)

DE Human parathyroid hormone analogue [Alb19]hPTH(1-34)NH₂.

KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;

OS bone fracture.

OS Homo sapiens.

OS Synthetic.

FT modified_site 19 Location/Qualifiers

FT modified_site 34 /label= Alb

FT modified_site 34 /note= "In amide form"

PD WO9702834-A1.

PF 30-JAN-1997.

PR 03-JUL-1996; U11292.

PR 13-JUL-1995; US-001105.

PR 06-SEP-1995; US-003305.

PR 29-MAR-1996; US-626186.

PA (BIO-M) BIOMEASURE INC.

PI Dong ZX.

DR WPI; 97-11819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which

PT stimulate bone growth and are used for treatment of osteoporosis and

PT bone fracture

PS Claim 11; Page -: 33pp; English.

CC The present sequence is a specific example of a human parathyroid

CC hormone (hPTH) analogue from fragment 1-34 in which at least one

CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34

CC is alpha-aminoisobutyric acid (Aib). In this example the Glu residue

CC at position 19 of the wild-type has been substituted by Aib. The hPTH

CC analogues stimulate bone growth and so are useful in human or veterinary

CC medicine for treatment of osteoporosis and bone fracture, optionally in

CC conjunction with anti-resorptive therapy (bisphosphonates and

CC calcitonin).

CC N.B. The present sequence does not appear in the specification. It

CC corresponds to the known hPTH 1-34 fragment with the modifications

CC as stated in the claim.

SO Sequence 34 AA.

Query Match 100.0%; Score 64; DB 22; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.96e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 nlghlnsm 18

QY 1 NLGRHLNSM 9

Search completed: Thu Jul 30 10:15:09 1998

Job time : 15 secs.

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE 15-25
 SUMMARY #length 34 #region helix (right hand alpha) #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 64; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.46e-03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 7 NLGKHLNSM 15
 QY 1 NLGKHLNSM 9

Search completed: Thu Jul 30 10:14:37 1998
 Job time : 19 secs.

WIDEORIT (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:13:18 1998; Maspar time 3.76 Seconds
Tabular output not generated. 100.904 Million cell updates/sec

Title: >US-08-817-547A-8
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 NLGKHLNSM 9

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.703; Variance 22.712; scale 0.956

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	50	78.1	105	10	063473	PARATHYROID HORMONE (F	5.27e-01
2	50	78.1	367	10	063778	HYPOTHETICAL 43.7 KD P	5.27e-01
3	50	78.1	513	10	063289	L1 RETROPOSON, ORF2 MR	5.27e-01
4	50	78.1	1300	10	P97692	L1 RETROTRANSPOSON ORF	5.27e-01
5	48	75.0	437	6	Q36379	ATP SYNTHASE A CHAIN (1.63e+00
6	47	73.4	421	9	Q28532	HYPOTHETICAL 48.5 KD P	2.84e+00
7	47	73.4	619	1	099234	CHROMOSOME XV READING	2.84e+00
8	46	71.9	472	3	009656	HYPOTHETICAL 52.6 KD P	4.91e+00
9	46	71.9	1708	9	026769	MAGNESIUM CHELATEASE SU	4.91e+00
10	45	70.3	186	9	025653	SITE-SPECIFIC RECOMBIN	8.41e+00
11	45	70.3	385	9	018326	HUNCHBACK GAP (FRAGMEN	8.41e+00
12	45	70.3	545	9	032006	YOKA PROTEIN.	8.41e+00
13	45	70.3	671	9	045597	FUNCTION UNKNOWN.	8.41e+00
14	44	68.8	82	4	Q29248	APOLIPROTEIN A-1 (FR	1.43e+01
15	44	68.8	242	11	080897	COMPLETE GENOME (FRAG	1.43e+01
16	44	68.8	301	11	070212	ENVELOPE GLYCOPROTEIN,	1.43e+01
17	44	68.8	325	9	026290	LACTATE DEHYDROGENASE.	1.43e+01
18	44	68.8	545	11	090054	ORF2.	1.43e+01
19	43	67.2	171	2	015093	PLAOGLOBIN (FRAGMENT)	2.40e+01
20	43	67.2	443	9	P76507	FROM BASES 2458322 TO	2.40e+01

21	43	67.2	518	12	013035	PROSAPOSIN.	2.40e+01
22	43	67.2	534	3	Q23651	ZK853.3.	2.40e+01
23	43	67.2	646	10	063779	HYPOTHETICAL 76.2 KD P	2.40e+01
24	43	67.2	719	3	017828	CORF8.2.	2.40e+01
25	43	67.2	745	10	P70565	PLAOGLOBIN.	2.40e+01
26	43	67.2	745	2	015151	PLAOGLOBIN.	2.40e+01
27	43	67.2	979	3	Q21962	SIMILAR TO GLYCINE DEH	2.40e+01
28	43	67.2	1854	10	065131	RAT LUNG-DERIVED L01 C	2.40e+01
29	43	67.2	2294	2	Q15265	PROTEIN TYROSINE PHOSP	2.40e+01
30	43	67.2	2317	10	063130	RAT LUNG-DERIVED C-ROS	2.40e+01
31	43	67.2	2338	10	063132	RAT HEART-DERIVED C-RO	2.40e+01
32	43	67.2	2340	10	064736	ROSI PROTOONCOGENE (C-	2.40e+01
33	43	67.2	2340	10	067705	ROSI PROTOONCOGENE (PR	2.40e+01
34	43	67.2	2450	10	062135	PROTEIN-TYROSINE PHOSP	2.40e+01
35	43	67.2	2460	10	064512	PROTEIN TYROSINE PHOSP	2.40e+01
36	43	67.2	2466	2	Q15264	PROTEIN TYROSINE PHOSP	2.40e+01
37	43	67.2	2466	2	Q16826	PROTEIN-TYROSINE-POSP	2.40e+01
38	43	67.2	2484	4	Q28006	BAL TYROSINE PHOSPHAT	2.40e+01
39	43	67.2	2485	2	Q15263	PROTEIN TYROSINE PHOSP	2.40e+01
40	43	67.2	2490	2	Q15923	PROTEIN TYROSINE PHOSP	2.40e+01
41	42	65.6	290	9	Q03086	REPLICATION PROTEIN A	4.00e+01
42	42	65.6	1071	11	P89047	POLYPROTEIN (FRAGMENT)	4.00e+01
43	42	65.6	2251	3	Q22190	T05A10.1.	4.00e+01
44	42	65.6	2589	11	Q66776	POLYPROTEIN.	4.00e+01
45	42	65.6	3896	11	P87514	PESTIVIRUS POLYPROTEIN	4.00e+01

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	105 AA.
ID 063473:			
AC 063473:			
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE PARATHYROID HORMONE (FRAGMENT).			
GN PTH.			
OS RATTUS NORVEGICUS (RAT).			
OC EUMARIOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC EUMARIOTA; RODENTIA.			
RN [1]			
RC SEQUENCE FROM N.A.			
RP TISSUE-THYROID, AND PARATHYROID;			
RA SCHMELZER H.J., GROSS G., WAYER H.;			
RL ADV. GENE TECHNOL. 21:228-229(1984).			
DR EMBL; M54875; G601933; -.			
FT NON TER			
FT SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;			
Query Match	78.1%;	Score 50;	DB 10;
Best local similarity	77.8%;	Pred. No. 5.27e-01;	
Matches 7;	Conservative 1;	Mismatches 1;	Indels 0;
Gaps 0;			
DB 31 NLGKHLASV 39			
OY 1 NLGKHLNSM 9			
RESULT 2	PRELIMINARY:	PRT:	367 AA.
ID 063778:			
AC 063778:			
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE HYPOTHETICAL 43.7 KD PROTEIN.			
OS RATTUS NORVEGICUS (RAT).			
OC EUMARIOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC EUMARIOTA; RODENTIA.			
RN [1]			
RC SEQUENCE FROM N.A.			
RP TISSUE-LIVER;			
RL MEDLINE; 87064324.			
RX D'AMEROSIO E., WAITKIN S.D., WINNEY F.R., SALEMME A., FURANO A.V.;			

RL MOL. CELL. BIOL. 6:411-424(1986).
 DR EMBL: M13100; G804811; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;

Query Match 78.1%; Score 50; DB 10; Length 367;
 Best Local Similarity 66.7%; Pred. No. 5,27e-01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 74 KIKKHLEHM 82
 QY 1 NLGRHLNSM 9

Search completed: Thu Jul 30 10:14:00 1998
 Job time : 42 secs.

MIPS

(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:12:53 1998; Maspar time 2.12 Seconds
106.569 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-8
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 NLGKHLNSM 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.743; Variance 23.428; scale 0.971

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	64	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.05e-04
2	60	93.8	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.35e-03
3	60	93.8	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.35e-03
4	53	82.8	115	1	PTHY_PIG PARATHYROID HORMONE PR	9.45e-02
5	50	78.1	115	1	PTHY_RAT PARATHYROID HORMONE PR	5.29e-01
6	46	71.9	152	1	HMG-SOYBN HMG-Y RELATED PROTEIN	4.71e+00
7	46	71.9	176	1	HMG-SOYBN HMG-Y RELATED PROTEIN	4.71e+00
8	46	71.9	192	1	SC72 YEAST TRANSCRIPTION INITIAT	4.71e+00
9	46	71.9	2068	1	CCGL DROME TRANSCRIPTION INITIAT	4.71e+00
10	45	70.3	208	1	YFYL ECOLI HYPOHETICAL 24.6 KD P	7.96e+00
11	45	70.3	700	1	PTPE_HUMAN PROTEIN-TYROSINE PHOSP	7.96e+00
12	45	70.3	985	1	NAH_YERST PROBABLE NA(+)/H(+) AN	7.96e+00
13	44	68.8	265	1	APAL_PIG APOLIPROTEIN A-1 PRE	1.33e+01
14	44	68.8	298	1	YHBY ECOLI HYPOHETICAL 33.2 KD P	1.33e+01
15	44	68.8	585	1	Y187 MYCGE HYPOHETICAL ABC TRANS	1.33e+01
16	44	68.8	936	1	YK2K YEAST HYPOHETICAL 106.5 KD	1.33e+01
17	44	68.8	2105	1	POAR_ASCVP GENOME POLYPROTEIN (CN	1.33e+01
18	43	67.2	139	1	STBH_PESBM PLASID STABILITY PROT	2.21e+01
19	43	67.2	187	1	ATPD_OOSI ATP SYNTHASE DELTA CNA	2.21e+01
20	43	67.2	313	1	LDH_MERJA L-LACTATE DEHYDROGENAS	2.21e+01
21	43	67.2	462	1	CISY_TETTH CITRATE SYNTHASE, MITO	2.21e+01
22	43	67.2	621	1	PLAK_MOUSE JUNCTION PLAKGLOBIN (2.21e+01
23	43	67.2	738	1	PLAK_XENLA JUNCTION PLAKGLOBIN (2.21e+01

RESULT	ID	PTHY_HUMAN	STANDARD:	PRT:	115 AA.	ALIGNMENTS
AC	24	21-JUL-1986 (REL. 01, CREATED)				
DT	25	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)				
DT	26	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	27	PARATHYROID HORMONE PRECURSOR (PARATHYRLIN) (PTH).				
GN	28	PTH.				
OS	29	HOMO SAPIENS (HUMAN).				
OC	30	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	31	EUPHERIA; PRIMATES.				
RN	32	[1]				
RP	33	SEQUENCE FROM N.A.				
RX	34	MEDLINE: 82150870.				
RA	35	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;				
RL	36	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).				
RN	37	[2]				
RP	38	SEQUENCE FROM N.A.				
RX	39	MEDLINE: 83169834.				
RA	40	VASICER T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J.;				
RL	41	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;				
RL	42	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).				
RN	43	[3]				
RP	44	SEQUENCE OF 26-37.				
RX	45	MEDLINE: 74174967.				
RA	46	JACOBS J.W., KEMPER B., NITAL H.D., HABENER J.F., POTTS J.T. JR.;				
RL	47	NATURE 249:155-157(1974).				
RN	48	[4]				
RP	49	SEQUENCE OF 32-68.				
RX	50	MEDLINE: 74111656.				
RA	51	NITAL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;				
RL	52	O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.;				
RL	53	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).				
RN	54	[5]				
RP	55	SEQUENCE OF 61-83 AND 84-115.				
RX	56	MEDLINE: 79082855.				
RA	57	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;				
RL	58	POTTS J.T. JR.;				
RL	59	BIOCHEMISTRY 17:5723-5729(1978).				
RN	60	[6]				
RP	61	SEQUENCE OF 75-100.				
RA	62	KEUTMANN H.T., NITAL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;				
RL	63	O'RIORDAN J.L.H., POTTS J.T. JR.;				
RL	64	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.;				
RL	65	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,				
RL	66	(1975).				
RN	67	[7]				

FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT CONFLICT 106 106
 SQ SEQUENCE 115 AA; 12980 MW; 673EASf2 CRC32;

Query Match 93.8%; Score 60; DB 1; Length 115;

Best Local Similarity 88.9%; Pred. No. 1.35e-03;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 41 NLGKHLSSM 49
 QY 1 NLGKHLNSM 9

Search completed: Thu Jul 30 10:12:59 1998
 Job time : 6 secs.



FT	SIGNAL	1	25	
FT	PROPEP	26	31	
FT	CHAIN	32	115	PARATHYROID HORMONE.
FT	CONFLICT	106	106	V -> G (IN REF. 4).
SO	SEQUENCE	115 AA;	12980 MW;	673EA5F2 CRC32;

Query Match 92.2%; Score 47; DB 1; Length 115;
 Best Local Similarity 83.7%; Pred. No. 1.19e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 43 GKHLISM 49
 ||||:||
 QY 1 GKHLISM 7

Search completed: Thu Jul 30 10:17:55 1998
 Job time : 8 secs.



COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15-25
 SUMMARY

#region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 59; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.45e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 LGRHLNSM 15
 |||||
 QY 1 LGRHLNSM 8

Search completed: Thu Jul 30 10:16:15 1998
 Job time : 24 secs.

RP REVISIONS.
RX MEDLINE: 75146516.
RA KEUTMANN H.T., NIALI H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
RL BIOCHEMISTRY 14:1842-1847(1975).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 75059220.
RA TREGGAR G.W., VAN RIENSCHOTEN J., GREEN E., NIALI H.D.,
RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 355:415-421(1974).
RN [9]
RX SYNTHESIS OF 32-65.
RX MEDLINE: 73227467.
RA ANDREATTA R.H., HARTMAN A., JOEHL A., KAMBER B., MAIER R.,
RA RINKER B., RITTEL W., STEBER P.;
RL HELV. CHIM. ACTA 56:470-473(1973).
RN [10]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 91299748.
KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
BIOCHEMISTRY 30:6936-6942(1991).
RN [11]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 93345518.
RA BARDEN J.A., CUTHERSON R.M.;
RL EUR. J. BIOCHEM. 215:315-321(1993).
RN [12]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE: 95318084.
RA MARX U.C., AUSTERMANN S., BAYER P., ADELMANN K., ECHART A.,
RA STICHT H., WALTER S., SCHMID F.X., JAENITKE R., FORSMANN W.-G.,
RA ROESCH P.;
RL J. BIOL. CHEM. 270:15194-15202(1995).
RN [13]
RP VARIANT ARG-18.
RX MEDLINE: 91009811.
RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
RA KRONENBERG H.M.;
RL J. CLIN. INVEST. 86:1084-1087(1990).
RN [14]
CC CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC HYPOPARATHYROIDISM (FTH).
CC EMBL: 300301; G190704; -
DR EMBL: V00597; G37144; -
DR EMBL: A29146; E186700; -
DR PIR: A01536; PTHU.
DR PIR: A19339; A19339.
DR PDB: 1HPH: 10-JUL-85.
DR PDB: 1HTI: 15-OCT-97.
DR PDB: 1ZWA: 12-MAR-97.
DR PDB: 1ZWB: 12-MAR-97.
DR PDB: 1ZWC: 12-MAR-97.
DR PDB: 1ZWD: 12-MAR-97.
DR PDB: 1ZWE: 12-MAR-97.
DR PDB: 1ZWF: 16-JUN-97.
DR PDB: 1ZWG: 16-JUN-97.
DR MIM: 146200; -
DR MIM: 168450; -
DR PROSITE: PS00335; PARATHYROID: 1.
KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT VARIANT 18 18
FT CONFLICT 107 107
SQ SEQUENCE 115 AA; 12861 MW; 243E87C7 CRC32;
Query Match 100.0%; Score 59; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 9,298-04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

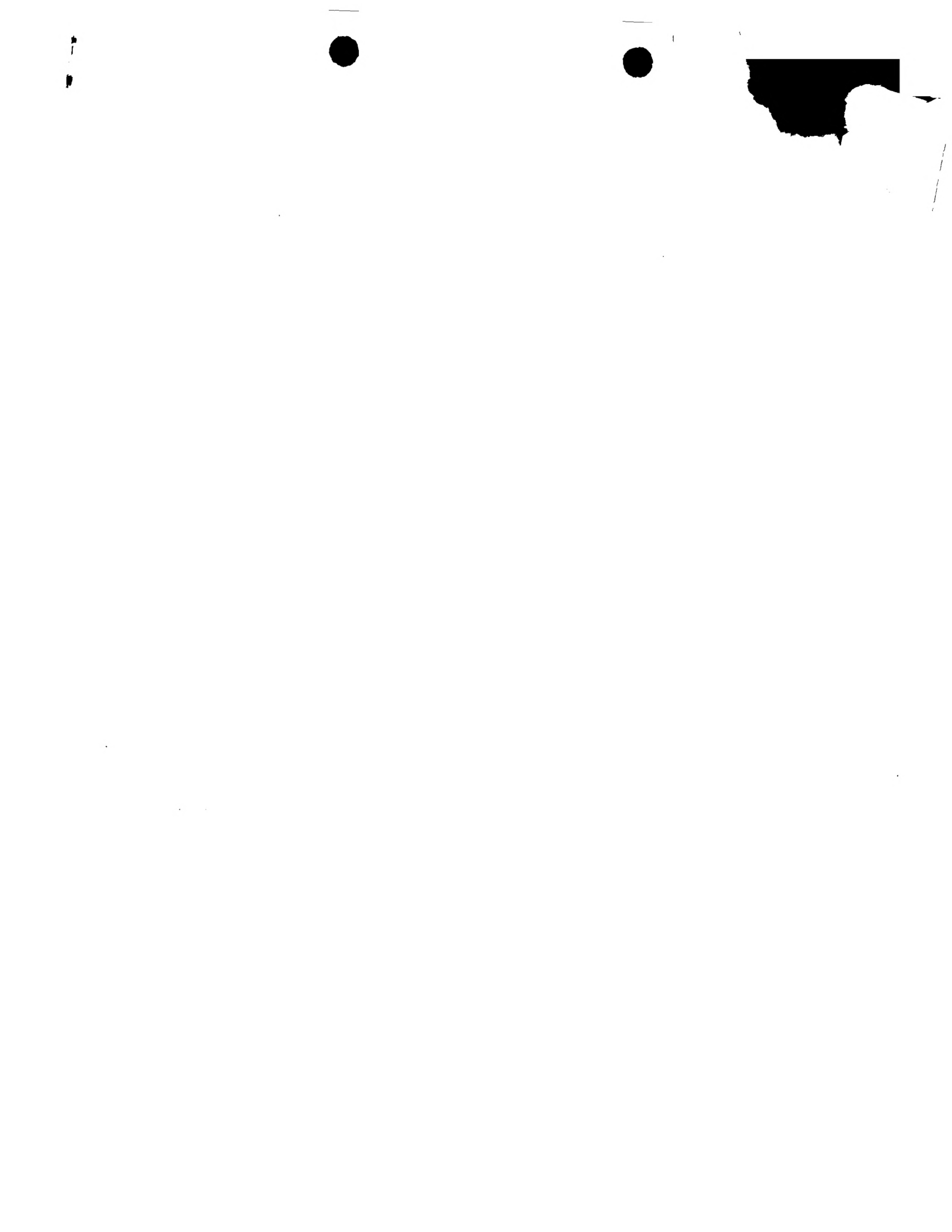
DB 42 LGKHLNSM 49
QY 1 LGKHLNSM 8
RESULT 2
ID PTHX_BOVIN STANDARD; PRT; 115 AA.
AC P01266;
DE 21-JUL-1986 (REL. 01, CREATED)
DE 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHIRIN) (PTH).
CN PTH.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RA POTTS J.T. JR., RICH A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALI H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RA COHN D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALI H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAMSON B.F.,
RA AURBACH G.D., POTTS J.T. JR.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREWER H.B. JR., ROMAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALI H.D., SAUER R.,
RA DEFLOS L.J., DAMSON B.F., HOGAN M.L., AURBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
RN [9]
CC CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: J00106; G85; -
DR EMBL: J00023; G163641; -
DR EMBL: J00024; G163643; -
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01398; G163647; -
DR EMBL: M25082; G163645; -
DR PIR: A01534; PTHO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID: 1.
KW HORMONE; SIGNAL.

FT SIGNAL 1 25
 FT PROPER 26 31
 FT CHAIN 32 115
 FT CONFLICT 106 106
 SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;
 PARATHYROID HORMONE.
 V -> G (IN REF. 4).

Query Match 93.2%; Score 55; DB 1; length 115;
 Best Local Similarity 87.5%; Pred. No. 1.20e-02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 42 LGKHLSSM 49
 |||||:
 OY 1 LGKHLNSM 8

Search completed: Thu Jul 30 10:15:34 1998
 Job time : 7 secs.





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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:16:32 1998; Maspar time 3.68 Seconds
Tabular output not generated. 91.451 Million cell updates/sec

Title: >US-08-817-547A-9
Description: (1-8) from US08817547A.pep
Perfect Score: 59
Sequence: 1 LGKHLNSM 8

Scoring table: PAM 150
Gap 15

Searched: 140542 segs. 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.247; Variance 21.504; scale 0.988
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	49	83.1	367	10	Q63778	HYPOTHETICAL 43.7 KD P	4.51e-01
2	49	83.1	513	10	Q63289	L1 RETROPOSON, ORF2 NR	4.51e-01
3	49	83.1	1300	10	P97692	L1 RETROTRANSPOSON ORF	4.51e-01
4	47	79.7	437	6	Q36379	ATP SYNTHASE A CHAIN (1.45e+00
5	46	78.0	472	3	Q09656	HYPOTHETICAL 52.6 KD P	2.58e+00
6	45	76.3	105	10	Q63473	PARATHYROID HORMONE (F	4.53e+00
7	45	76.3	545	9	Q33006	YOKA PROTEIN	4.53e+00
8	44	74.6	82	4	Q28248	APOLIPOPROTEIN A-I (FR	7.90e+00
9	44	74.6	242	11	Q80897	COMPLETE GENOME (FRAG	7.90e+00
10	44	74.6	301	11	Q70212	ENVELOPE GLYCOPROTEIN	7.90e+00
11	44	74.6	325	9	Q26290	LACTATE DEHYDROGENASE	7.90e+00
12	44	74.6	619	1	Q09234	CHROMOSOME XV READING	7.90e+00
13	44	74.6	671	9	Q45597	FUNCTION UNKNOWN	7.90e+00
14	43	72.9	171	2	Q15093	PLAKOGLOBIN (FRAGMENT)	1.36e+01
15	43	72.9	554	3	Q23651	ZK863.3	1.36e+01
16	43	72.9	719	3	Q17828	C08F8.2	1.36e+01
17	43	72.9	745	2	Q15151	PLAKOGLOBIN	1.36e+01
18	43	72.9	745	10	P70565	PLAKOGLOBIN	1.36e+01
19	43	72.9	1708	9	Q26769	MAGNESIUM CHELATASE SU	1.36e+01
20	42	71.2	107	10	Q60549	GROWTH HORMONE-RELEASE	2.33e+01

21	42	71.2	226	11	P89049	E0/E2 (FRAGMENT)	2.33e+01
22	42	71.2	278	9	Q55106	HOMOLOGUE TO PROTEIN E	2.33e+01
23	42	71.2	290	9	Q03086	REPLICATION PROTEIN A	2.33e+01
24	42	71.2	362	9	Q05512	BACILLUS SP. NANNAN EN	2.33e+01
25	42	71.2	363	9	Q29112	IRON-SULFUR CLUSTER BI	2.33e+01
26	42	71.2	421	9	Q28532	HYPOTHETICAL 48.5 KD P	2.33e+01
27	42	71.2	439	8	Q41770	ALPHA-AMYLASE	2.33e+01
28	42	71.2	518	12	Q13035	PROSAPIN	2.33e+01
29	42	71.2	646	10	Q63779	HYPOTHETICAL 76.2 KD P	2.33e+01
30	42	71.2	762	9	Q25338	DNA MISMATCH REPAIR PR	2.33e+01
31	42	71.2	825	8	Q22224	T3266.14 PROTEIN	2.33e+01
32	42	71.2	979	3	Q21962	SIMILAR TO GLYCINE DEH	2.33e+01
33	42	71.2	1067	11	Q65447	STRUCTURAL POLYPEPTIDE	2.33e+01
34	42	71.2	1071	11	P89047	POLYPEPTIDE (FRAGMENT)	2.33e+01
35	42	71.2	2294	2	Q15265	PROTEIN TYROSINE PHOSP	2.33e+01
36	42	71.2	2450	10	Q62135	PROTEIN TYROSINE PHOSP	2.33e+01
37	42	71.2	2460	10	Q64512	PROTEIN TYROSINE PHOSP	2.33e+01
38	42	71.2	2466	10	Q15264	PROTEIN TYROSINE PHOSP	2.33e+01
39	42	71.2	2466	2	Q16826	PROTEIN-TYROSINE-PHOSP	2.33e+01
40	42	71.2	2484	4	Q28006	BAL4 TYROSINE PHOSPHAT	2.33e+01
41	42	71.2	2485	2	Q15263	PROTEIN TYROSINE PHOSP	2.33e+01
42	42	71.2	2490	2	Q12923	PROTEIN TYROSINE PHOSP	2.33e+01
43	42	71.2	3896	11	P87514	PESTIVIRUS POLYPEPTIDE	2.33e+01
44	41	69.5	164	12	Q92037	NITRIC-OXIDE SYNTHASE	3.94e+01
45	41	69.5	545	11	Q90054	ORF2	3.94e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	367 AA
AC	Q63778			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	HYPOTHETICAL 43.7 KD PROTEIN			
OS	RATTUS NORVEGICUS (RAT)			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER:			
RX	MEDLINE: 87064324.			
RA	D'AMBROSIO E., WAITZKIN S.D., WITNEY F.R., SALEME A., FURANO A.V.:			
RL	MOL. CELL. BIOL. 6:411-424(1986).			
DR	EMBL: M13100; G804811; -			
KW	HYPOTHETICAL PROTEIN.			
SO	SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;			
Query Match				
Best Local Similarity 75.0%; Score 49; DB 10; Length 367;				
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
DB	75 LGKHLNSM 82			
OY	1 LGKHLNSM 8			
RESULT 2				
ID	Q63289	PRELIMINARY	PRT	513 AA.
AC	Q63289			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	L1 RETROPOSON, ORF2 MRNA (PARTIAL) (FRAGMENT).			
OS	RATTUS NORVEGICUS (RAT)			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
CC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER:			
RX	MEDLINE: 92375092.			
RA	ILYES H., KAIRE O., SPEEK M.:			

Thu Jul 30 13:38:23 1998

US-08-817-547A-9.rspt

Page 2

RL MOL. CELL. BIOL. 12:4242-4248(1992).
DR EMBL: X61295; G56322; .
FT NON TER 1

SQ SEQUENCE 513 AA; 60414 MW; 3EB70B62 CRC32;

Query Match 83.1%; Score 49; DB 10; Length 513;
Best Local Similarity 75.0%; Pred. NO. 4.51e-01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 423 IGRHLEHM 430

OY 1 IGRHLSM 8

Search completed: Thu Jul 30 10:16:53 1998
Job time : 21 secs.

WIDEORH (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:20:02 1998; MasPar time 2.67 Seconds
40.289 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-10
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 GKHLNSM 7

Scoring table:
PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.516; Variance 40.392; scale 0.359

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of chance being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	51	100.0	27	3	P82185	Sequence of parathyro 1.10e+01
2	51	100.0	34	22	W17939	Human parathyroid hor 1.10e+01
3	51	100.0	34	22	W17954	Human parathyroid hor 1.10e+01
4	51	100.0	34	22	W17955	Human parathyroid hor 1.10e+01
5	51	100.0	34	22	W17950	Human PTH analogue [C 1.10e+01
6	51	100.0	34	7	R34355	Human parathyroid hor 1.10e+01
7	51	100.0	34	22	W17962	Human PTH analogue [C 1.10e+01
8	51	100.0	34	22	W17951	Human parathyroid hor 1.10e+01
9	51	100.0	34	19	R98951	Target peptide (PTH(1 1.10e+01
10	51	100.0	34	22	W17943	Human parathyroid hor 1.10e+01
11	51	100.0	34	22	W17944	Human parathyroid hor 1.10e+01
12	51	100.0	34	22	W17947	Human parathyroid hor 1.10e+01
13	51	100.0	36	9	R58243	Properlyl-[Al]-hPTH(1 1.10e+01
14	51	100.0	36	9	R58177	[Morpholine-2-carboxy 1.10e+01
15	51	100.0	36	9	R58170	[Nval]-hPTH(1-36)-NH2 1.10e+01
16	51	100.0	36	9	R58267	[Phe8]-hPTH(1-36)-NH2 1.10e+01
17	51	100.0	36	9	R58268	[Cha8]-hPTH(1-36)-NH2 1.10e+01
18	51	100.0	36	9	R58229	[Ala30]-hPTH(1-36)-NH 1.10e+01
19	51	100.0	36	9	R58026	N-alpha-methyl[Ala1] 1.10e+01

20	51	100.0	37	9	R58244	[Ala0]-hPTH(1-36)-NH2 1.10e+01
21	51	100.0	38	9	R58141	[Leu21]-hPTH(1-38)-OH 1.10e+01
22	51	100.0	38	9	R58145	[Gly22]-hPTH(1-38)-OH 1.10e+01
23	51	100.0	38	9	R58075	[Ser33]-hPTH(1-38)-OH 1.10e+01
24	51	100.0	38	9	R58078	[Gly33]-hPTH(1-38)-OH 1.10e+01
25	51	100.0	38	19	R98958	Target peptide (PTH(1 1.10e+01
26	51	100.0	38	9	R58128	[Met19]-hPTH(1-38)-OH 1.10e+01
27	51	100.0	44	26	P30015	Human parathyroid hor 1.10e+01
28	51	100.0	47	25	W21946	Fusion protein compit 1.10e+01
29	51	100.0	84	27	W25687	Human parathyroid hor 1.10e+01
30	51	100.0	84	27	R21180	Human parathyroid hor 1.10e+01
31	51	100.0	84	4	R21181	Human parathyroid hor 1.10e+01
32	51	100.0	84	4	R21220	Human parathyroid hor 1.10e+01
33	51	100.0	84	4	R23226	Human parathyroid hor 1.10e+01
34	51	100.0	84	4	R23523	Human parathyroid hor 1.10e+01
35	51	100.0	84	7	R34460	Human parathyroid hor 1.10e+01
36	51	100.0	84	4	R21227	Human parathyroid hor 1.10e+01
37	51	100.0	84	4	R21226	Human parathyroid hor 1.10e+01
38	51	100.0	84	25	W29420	Human parathyroid hor 1.10e+01
39	51	100.0	84	4	R23229	Human parathyroid hor 1.10e+01
40	51	100.0	84	4	R23243	Human parathyroid hor 1.10e+01
41	51	100.0	84	4	R21197	Human parathyroid hor 1.10e+01
42	51	100.0	84	4	R23237	Human parathyroid hor 1.10e+01
43	51	100.0	84	4	R21218	Human parathyroid hor 1.10e+01
44	51	100.0	84	4	R21219	Human parathyroid hor 1.10e+01
45	51	100.0	84	9	R49694	Sequence of variant o 1.10e+01

ALIGNMENTS

RESULT 1
ID P82185 standard; Protein: 27 AA.

AC P82185;
DT 06-MAR-1992 (first entry)
DE Sequence of parathyroid hormone (PTH) analogue [L-Phe23]hPTH(7-34)NH2.
KW Parathyroid hormone analogue; osteoporosis therapy; hypercalcaemia;
KM hyperparathyroidism; hormone dependent tumour; bioassay; diagnosis;
treatment.
OS Homo sapiens.
PN US4771124-A.
PD 13-SEP-1988.
PF 26-MAY-1987; 054359.
PR 26-MAY-1987; US-054359.
PA (MERT) MERCK & CO INC.
PI Rosenblatt M, Caporale LH, Nutt RF, Levy JJ, Chorev M;
DR WPI: 88-278169/39.
PT Parathyroid hormone peptide analogues - used for treating
PT osteoporosis, hypercalcaemia, hyperparathyroidism and hormone
PT dependent tumours, and in vitro for bioassays
PS Clam 5; column 8; 5pp; English.
CC The PTH analogues of the invention are used for inhibiting the
CC naturally-occurring hormone in vivo and in vitro. They have high
CC binding affinity for their resp. cell surface receptors while not
CC stimulating prodn. of second messenger molecules. They may be used
CC in vitro in a bioassay for PTH and in vivo for therapy and diagnosis.
CC They are prepd. in dosage forms for oral, parenteral, rectal, intra-
CC nasal or topical admin.
SQ Sequence 27 AA;

Query Match 100.0%; Score 51; DB 3; Length 27;
Best local Similarity 100.0%; Pred. No. 1.10e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 gkhlsm 12
|||
QY 1 GKHLNSM 7

RESULT 2
ID W17939 standard; peptide; 34 AA.
AC W17939;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.

```

KM Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.
OS Homo sapiens.
OS Synthetic.
FH Key
FT modified_site 7 Location/Qualifiers
FT modified_site 11 /label= OTHER
FT modified_site 11 /note= "Cyclohexylalanine (Cha)"
FT modified_site 11 /label= OTHER
FT modified_site 34 /note= "Cha"
FT modified_site 34 /note= "In amide form"
FT modified_site 34 /note= "In amide form"
PN WO9702834-A1.
PD 30-JAN-1997.
PF 03-JUL-1996; U11292.
PR 13-JUL-1995; US-001105.
PR 06-SEP-1995; US-003305.
PR 29-MAR-1996; US-626186.
PR (BIOM-) BIOMEDASURE INC.
Dong ZX;
WPI; 97-118819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which
PT stimulate bone growth and are used for treatment of osteoporosis and
PT bone fracture
PS Claim 5; Page -: 33pp; English.
CC The present sequence is a specific example of a human parathyroid
CC hormone (hPTH) analogue from fragment 1-34 in which at least one
CC of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31
CC is cyclohexylalanine (Cha). In this example the Leu residue at
CC position 7 and the Leu at position 11 in the wild-type have been
CC substituted by Cha. The hPTH analogues stimulate bone growth and so
CC are useful in human or veterinary medicine for treatment of
CC osteoporosis and bone fracture, optionally in conjunction with
CC anti-resorptive therapy (bisphosphonates and calcitonin).
CC N.B. The present sequence does not appear in the specification. It
CC corresponds to the known hPTH 1-34 fragment with the modifications
CC as stated in the claim.
SQ Sequence 34 AA;

Query Match 100.0%; Score 51; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.10e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 gkhlnsm 18
| | | | | | |
QY 1 GKHLNSM 7

Search completed: Thu Jul 30 10:20:20 1998
Job time : 18 secs.

```

 WISE (TM)

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Msrch_Pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:19:17 1998; Maspar time 3.25 Seconds
 Tabular output not generated. 78.689 Million cell updates/sec

Title: >US-08-817-547A-10
 Description: (1-7) from US08817547A.pep
 Perfect Score: 51
 Sequence: 1 GKHLNSM 7

Scoring table: PAM 150
 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: plr56
 1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 19.845; Variance 21.817; scale 0.910
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	51	100.0	34	5	12WA parathyroid hormone (8.41e-02	
2	51	100.0	34	5	12WE parathyroid hormone (8.41e-02	
3	51	100.0	34	5	12WG parathyroid hormone 4 8.41e-02	
4	51	100.0	34	5	12WF parathyroid hormone 4 8.41e-02	
5	51	100.0	35	5	12WD parathyroid hormone (8.41e-02	
6	51	100.0	36	5	12WB parathyroid hormone (8.41e-02	
7	51	100.0	37	5	12WB parathyroid hormone (8.41e-02	
8	51	100.0	37	5	12WB parathyroid hormone (8.41e-02	
9	51	100.0	37	5	12WB parathyroid hormone (8.41e-02	
10	47	92.2	115	2	JC4202 parathyroid hormone (8.32e-01	
11	47	92.2	115	1	PTBO parathyroid hormone p 4.31e+00	
12	44	86.3	2105	1	A44059 RNA-directed RNA poly 8.32e-01	
13	42	82.4	362	2	H69785 mannan endo-1,4-beta- 1.24e+01	
14	42	82.4	363	2	H69393 iron-sulfur cluster b 1.24e+01	
15	42	82.4	501	2	S45914 glucan 1,3-beta-gluc 1.24e+01	
16	41	80.4	421	2	D69981 conserved hypochetica 2.08e+01	
17	41	80.4	513	2	S21976 probable RNA-directed 2.08e+01	
18	41	80.4	558	2	S61604 probable membrane pro 2.08e+01	
19	41	80.4	3005	2	S33642 homeotic protein zif- 3.45e+01	
20	40	78.4	115	1	PTPG parathyroid hormone p 3.45e+01	
21	40	78.4	545	1	B44054 orf2 protein - Junon 3.45e+01	
22	40	78.4	690	2	A24545 triacylglycerol lipas 3.45e+01	
23	39	76.5	176	2	I84638 pituitary adenylate c 5.67e+01	

24	39	76.5	263	2	B59807 polysaccharide deacet	5.67e+01
25	39	76.5	318	2	F38888 CoI Intron 13 protein	5.67e+01
26	39	76.5	356	2	S39889 SMI protein - Podosp	5.67e+01
27	39	76.5	377	2	S61892 outer membrane protei	5.67e+01
28	39	76.5	437	2	S52014 atp6 protein - common	5.67e+01
29	39	76.5	437	2	S48853 H++transporting ATP s	5.67e+01
30	39	76.5	587	2	S61038 D-lactate dehydrogena	5.67e+01
31	39	76.5	648	2	S61167 cyck protein homolog	5.67e+01
32	39	76.5	662	2	S61193 probable membrane pro	5.67e+01
33	38	74.5	152	2	S22311 HMG-Y-related protein	9.24e+01
34	38	74.5	176	2	S22310 HMG-Y-related protein	9.24e+01
35	38	74.5	181	2	A64393 hypothetical protein	9.24e+01
36	38	74.5	193	2	A53835 SE663 protein complex	9.24e+01
37	38	74.5	290	2	A36134 REPA protein - Escher	9.24e+01
38	38	74.5	545	2	E69907 DNA recombinase homol	9.24e+01
39	38	74.5	670	2	S47042 protein kinase (EC 2.	1.49e+02
40	37	72.5	193	2	E69469 hypothetical protein	1.49e+02
41	37	72.5	253	1	PMHUYM phosphoglycerate muta	1.49e+02
42	37	72.5	295	5	2AT2A aspartate transcardam	1.49e+02
43	37	72.5	295	5	2AT2B aspartate transcardam	1.49e+02
44	37	72.5	295	5	2AT2C aspartate transcardam	1.49e+02
45	37	72.5	491	2	I40991 signal transducer amp	1.49e+02

ALIGNMENTS

RESULT 1
 ENTRY 12WA #type complete
 TITLE parathyroid hormone (residues 1-34) - human
 ALTERNATE_NAMES HPTH(1-34)
 PDB_TITLE structure of human parathyroid hormone fragment 1-34, NMR 10
 ORGANISM #formal_name Homo sapiens #common_name man
 REFERENCE A67856
 #authors Roesch, P.; Marx, U.C.
 #submission submitted to the Brookhaven Protein Data Bank, June 1996
 #cross-References PDB:12WA
 REFERENCE TN001717
 #authors Marx, U.C.
 #book In Strukturen Verschiedener Parathormonfragmente In Loesung,
 pp.0, Bayreuth : University of Bayreuth (thesis), 1996
 COMMENT Resolution: not applicable
 KEYWORDS Determination: NMR
 FEATURE hormone
 SUMMARY 6-9 #region helix (right hand alpha) \
 19-30 #region helix (right hand alpha)
 #length 34 #molecular-weight 4118 #checksum 5629

Query Match 100.0%; Score 51; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8.41e-02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 12 GKHLNSM 18
 Qy 1 GKHLNSM 7
 RESULT 2
 ENTRY 12WE #type complete
 TITLE parathyroid hormone (residues 4-37) - human
 ALTERNATE_NAMES HPTH(4-37)
 PDB_TITLE structure of human parathyroid hormone fragment 4-37, NMR 10
 ORGANISM #formal_name Homo sapiens #common_name man
 REFERENCE A67860
 #authors Roesch, P.; Marx, U.C.
 #submission submitted to the Brookhaven Protein Data Bank, June 1996
 #cross-References PDB:12WE
 REFERENCE TN001721
 #authors Marx, U.C.
 #book In Strukturen Verschiedener Parathormonfragmente In Loesung,
 pp.0, Bayreuth : University of Bayreuth (thesis), 1996

Thu Jul 30 13:37:53 1998

US-08-817-547A-10.rpr






Page 2

COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS hormone
FEATURE 15-25
SUMMARY

#region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 51; DB 5; length 34;
Best Local Similarity 100.0%; Pred. No. 8.41e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 9 GKRLNSM 15
QY 1 GKRLNSM 7

Search completed: Thu Jul 30 10:19:45 1998
Job time : 28 secs.

RP REVISIONS.
 RX MEDLINE; 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 75059220.
 RA TREGGAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 73227467.
 RA ANDRETTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA RINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 93345518.
 RA BARDEEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE; 95318084.
 RA MARX U.C., AUSTERMANN S., BAYER P., ADERMAN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE; 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FIH).
 CC EMBL; J00301; G190704; -.
 DR EMBL; V00597; G37144; -.
 DR EMBL; A29146; E186700; -.
 DR PIR; A01536; PTHU.
 DR PIR; A19339; A19339.
 DR PDB; 1HPH; 10-JUL-95.
 DR PDB; 1HTH; 15-OCT-97.
 DR PDB; 12WA; 12-MAR-97.
 DR PDB; 12WB; 12-MAR-97.
 DR PDB; 12WC; 12-MAR-97.
 DR PDB; 12MD; 12-MAR-97.
 DR PDB; 12WE; 12-MAR-97.
 DR PDB; 12WF; 16-JUN-97.
 DR PDB; 12WG; 16-JUN-97.
 DR MIM; 146200; -.
 DR MIM; 168450; -.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT STGALP 26 31
 FT STGALP 32 115
 FT CHAIN 18 18
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA; 12861 MW; 24387C7 CRC32;
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 Query Match 100.0%; Score 51; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 7.72e-03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 GKHLNSM 49
 QY 1 GKHLNSM 7
 RESULT 2
 ID PTH_BOVIN STANDARD; PRT; 115 AA.
 AC P01268;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHIRIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 80056617.
 RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
 RA POTTS J.T. JR., RICH A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82037785.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83105964.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 84262483.
 RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
 RL GENE 28:319-322(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE; 74142666.
 RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
 RA COHN D.V.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
 RN [6]
 RP SEQUENCE OF 32-115.
 RX MEDLINE; 71076162.
 RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
 RA AURBACH G.D., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
 RN [7]
 RP SEQUENCE OF 32-115.
 RX MEDLINE; 71063634.
 RA BREWER H.B. JR., RONAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 71091588.
 RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
 RA DEFLOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL; V00106; G85; -.
 DR EMBL; J00023; G163641; -.
 DR EMBL; J00024; G163643; -.
 DR EMBL; J00024; E18249; ALT_SEQ.
 DR EMBL; J00024; E18250; ALT_SEQ.
 DR EMBL; K01938; G163647; -.
 DR EMBL; M25082; G163645; -.
 DR PIR; A01536; PTHO.
 DR PIR; A24949; A24949.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.

WIDEORH

(TM)

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Search_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:18:13 1998; Maspar time 3.99 Seconds
73.877 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-10
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 GKHLNSM 7

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 19.774; Variance 18.165; scale 1.089

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description	Pred. No.
1	43	84.3	719	3	017828	COBF8.2.	1.84e+00
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3	42	82.4	363	9	029112	IRON-SULFUR CLUSTER BI	3.42e+00
4	41	80.4	75	7	038347	ORF75.	6.31e+00
5	41	80.4	367	10	063728	HYPOHETICAL 43.7 KD P	6.31e+00
6	41	80.4	421	9	034528	YRVN PROTEIN.	6.31e+00
7	41	80.4	513	10	063289	LI RETROPOSON, ORF2 MR	6.31e+00
8	41	80.4	1072	2	015101	ZINC FINGER HOMEODOMAI	6.31e+00
9	41	80.4	1300	10	P97692	LI RETROTRANSPOSON ORF	6.31e+00
10	41	80.4	3703	2	015911	ZINC FINGER HOMEODOMAI	6.31e+00
11	41	80.4	3726	10	061329	AT MOTIF BINDING FACTO	6.31e+00
12	40	78.4	545	11	090054	ORF2.	1.15e+01
13	39	76.5	39	11	065545	EBV B95-8 CC(E) DNA WI	2.07e+01
14	39	76.5	143	7	003935	MINOR CAPSID PROTEIN.	2.07e+01
15	39	76.5	242	3	018238	Y57G11C.14.	2.07e+01
16	39	76.5	263	9	034928	YFUS PROTEIN.	2.07e+01
17	39	76.5	318	6	002684	HYPOHETICAL 36.5 KD P	2.07e+01
18	39	76.5	437	6	036379	ATP SYNTHASE A CHAIN (2.07e+01
19	39	76.5	643	3	022010	R186.4.	2.07e+01
20	39	76.5	3429	3	024593	X GENE.	2.07e+01

21	38	74.5	181	9	058155	HYPOTHETICAL 21.1 KD P	3.69e+01
22	38	74.5	290	9	003086	REPLICATION PROTEIN A	3.69e+01
23	38	74.5	315	3	021593	HYPOTHETICAL 36.4 KD P	3.69e+01
24	38	74.5	367	9	045125	MOBILIZATION PROTEIN.	3.69e+01
25	38	74.5	439	8	041770	ALPHA-AMYLASE	3.69e+01
26	38	74.5	472	3	009656	HYPOTHETICAL 52.6 KD P	3.69e+01
27	38	74.5	545	9	032006	YOKA PROTEIN.	3.69e+01
28	38	74.5	686	3	P92006	MO4G12.3.	3.69e+01
29	38	74.5	711	9	P95539	CATALASE (EC 1.11.1.6)	3.69e+01
30	38	74.5	719	3	025826	CDG2-RELATED PROTEIN K	3.69e+01
31	38	74.5	1258	3	010908	HYPOTHETICAL 140.5 KD	3.69e+01
32	38	74.5	1372	3	P91526	SIMILARITY TO MULTIPLE	3.69e+01
33	37	72.5	99	9	053074	UVRB (FRAGMENT).	6.49e+01
34	37	72.5	105	10	063473	PARATHYROID HORMONE (F	6.49e+01
35	37	72.5	193	9	028516	HYPOTHETICAL 22.0 KD P	6.49e+01
36	37	72.5	196	9	006737	PUTATIVE - POSSIBLE PH	6.49e+01
37	37	72.5	247	9	007821	SULFIDE-DEHYDROGENASE	6.49e+01
38	37	72.5	258	8	023434	HYPOTHETICAL PROTEIN.	6.49e+01
39	37	72.5	271	1	008558	CHROMOSOME XV READING	6.49e+01
40	37	72.5	518	12	013035	PROSAPOSIN.	6.49e+01
41	37	72.5	573	11	010621	CHITINASE.	6.49e+01
42	37	72.5	585	11	007041	G3R PROTEIN.	6.49e+01
43	37	72.5	646	11	037319	NUCLEOSIDE TRIPHOSPHAT	6.49e+01
44	37	72.5	940	1	007048	RNA POLYMERASE (FRAGME	6.49e+01
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ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	719 AA.
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DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DI	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
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RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	HARRIS B.			
RL	SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94150718.			
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,			
RA	BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,			
RA	CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,			
RA	GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,			
RA	JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,			
RA	LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,			
RA	PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SANDERS D., SHOWNKEEN R.,			
RA	SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,			
RA	THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,			
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.,			
RL	NATURE 368:32-38(1994).			
DR	EMBL; 273103; E242596; -			
SO	SEQUENCE 719 AA; 81009 MW; E206BB38 CRC32;			
Query Match		84.3%;	Score 43;	DB 3; Length 719;
Best Local Similarity		71.4%;	Pred. No. 1.84e+00;	
Matches	5; Conservative	2; Mismatches	0; Indels	0; Gaps 0;
Db	637 SKHLDSM 643			
QY	1 GKHLNSM 7			
RESULT	2	PRELIMINARY:	PRT:	362 AA.
ID	005512			
AC	005512;			
DT	01-JUL-1997 (TREMBLREL. 04, CREATED)			
DT	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)			

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE BACILLUS SP. MANNAN ENDO-1.
 GN YDHT.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA SADAIE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
 RL OOGASAWARA N.,
 RN SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA SADAIE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
 RL OOGASAWARA N.,
 RN SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RP [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA KUNST F., OOGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
 AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
 BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
 BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
 CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
 ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOUGER D.,
 FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
 GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
 GUISEPPI G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A.,
 HILBERT H., HOSAPPEL S., HOSONO S., HUULO M.F., ITAYA M., JONES L.,
 JORIS B., KARAWATA D., KASAHARA Y., KLAER-BLANCHARD M., KLEIN C.,
 KOBAYASHI Y., KOETTER P., KONIGSTEIN G., KROGH S., KUMANO M.,
 KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
 KURITA K., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
 MEDINA N., MELIADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 NOONE D., O'REILLY M., OGAWA K., OGIMARA A., OUDEGA B., PARK S.H.,
 PARO V., POHL T.M., PORTELELLA D., FORNOLIK S., PRESCOTT A.M.,
 PRESCAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
 RIEGER M., RIYOLTA C., ROCHA E., ROCHE R., ROSE M., SADAIE Y.,
 SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOPFONE F.,
 SEKIGUCHI J., SEROWSKA A., SEROR S.J., SEROR P., SHIN B.S., SOLDO B.,
 SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
 TAKUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
 TOSATO V., UCHIYAMA S., VANDEBOL M., VANNTER F., VASSAROTI A.,
 VIARI A., WAMBUUT R., WEDLER E., WEDLER H., WEITZENGGER T.,
 WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
 YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
 RN NATURE 390:249-256(1997).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA KUNST F., OOGASAWARA N., YOSHIKAWA H., DANCHIN A.,
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: D88802; D1020491; -;
 DR EMBL: 299107; E1182567; -;
 SQ SEQUENCE 362 AA; 40834 MW; 616962F9 CRC32;

Query Match 82.4%; Score 42; DB 9; Length 362;
 Best Local Similarity 71.4%; Pred. No. 3.42e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 162 GKRLNAM 168
 QY 1 GKRLNSM 7

Search Completed: Thu Jul 30 10:18:58 1998
 Job time : 45 secs.



(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:22:22 1998; MasPar time 2.66 Seconds
34.605 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-11
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 KHLNSM 6

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.509; Variance 37.219; scale 0.363

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	44	100.0	34	22	W17968	Human parathyroid hor	4.47e+01
2	44	100.0	34	22	W17939	Human parathyroid hor	4.47e+01
3	44	100.0	34	22	W17935	Human parathyroid hor	4.47e+01
4	44	100.0	34	22	W17954	Human parathyroid hor	4.47e+01
5	44	100.0	34	22	W17969	Human parathyroid hor	4.47e+01
6	44	100.0	34	22	W17951	Human parathyroid hor	4.47e+01
7	44	100.0	34	8	R41537	[Gln25,26,27]hPTH (1-	4.47e+01
8	44	100.0	34	19	R89951	Target peptide (PTH(1-	4.47e+01
9	44	100.0	34	22	W17943	N-alpha-isopropyl-hPT	4.47e+01
10	44	100.0	34	22	W17944	Human parathyroid hor	4.47e+01
11	44	100.0	34	22	W17947	Human parathyroid hor	4.47e+01
12	44	100.0	34	22	W17947	Human parathyroid hor	4.47e+01
13	44	100.0	36	9	R58262	[Ala1]-hPTH(1-36)-NH2	4.47e+01
14	44	100.0	36	9	R58026	N-alpha-methyl[Ala1]	4.47e+01
15	44	100.0	36	9	R58243	Propargyl-[Ala1]-hPTH(1	4.47e+01
16	44	100.0	36	9	R58267	[Phe8]-hPTH(1-36)-NH2	4.47e+01
17	44	100.0	36	9	R58268	[Cha8]-hPTH(1-36)-NH2	4.47e+01
18	44	100.0	36	9	R58230	[D-Val131]-hPTH(1-36)-	4.47e+01
19	44	100.0	37	9	R58244	[Ala0]-hPTH(1-36)-NH2	4.47e+01

20	44	100.0	38	9	R58141	[Leu21]-hPTH(1-38)-OH	4.47e+01
21	44	100.0	38	9	R58147	[His22]-hPTH(1-38)-OH	4.47e+01
22	44	100.0	38	9	R58128	[Met19]-hPTH(1-38)-OH	4.47e+01
23	44	100.0	38	9	R58132	[Pro19]-hPTH(1-38)-OH	4.47e+01
24	44	100.0	38	19	R38958	Target peptide (PTH(1	4.47e+01
25	44	100.0	44	26	P30015	Human parathyroid hor	4.47e+01
26	44	100.0	47	25	W21946	Fusion protein compit	4.47e+01
27	44	100.0	78	6	R30859	Leu8 hPTH (7-84) mute	4.47e+01
28	44	100.0	81	6	R30854	hPTH mutein lacking 3	4.47e+01
29	44	100.0	84	27	W25687	Human parathyroid hor	4.47e+01
30	44	100.0	84	27	R21210	Human parathyroid hor	4.47e+01
31	44	100.0	84	4	R23232	Human parathyroid hor	4.47e+01
32	44	100.0	84	4	R23526	Human parathyroid hor	4.47e+01
33	44	100.0	84	4	R23235	Human parathyroid hor	4.47e+01
34	44	100.0	84	4	R23523	Human parathyroid hor	4.47e+01
35	44	100.0	84	4	R21209	Human parathyroid hor	4.47e+01
36	44	100.0	84	25	W29420	Human parathyroid hor	4.47e+01
37	44	100.0	84	4	R21253	Human parathyroid hor	4.47e+01
38	44	100.0	84	4	R21161	Human parathyroid hor	4.47e+01
39	44	100.0	84	4	R21160	Human parathyroid hor	4.47e+01
40	44	100.0	84	4	R21236	Human parathyroid hor	4.47e+01
41	44	100.0	84	4	R21254	Human parathyroid hor	4.47e+01
42	44	100.0	84	4	R21218	Human parathyroid hor	4.47e+01
43	44	100.0	84	4	R23227	Human parathyroid hor	4.47e+01
44	44	100.0	84	4	R23231	Human parathyroid hor	4.47e+01
45	44	100.0	84	4	R21153	Human parathyroid hor	4.47e+01

ALIGNMENTS

RESULT 1
ID W17968 standard; peptide; 34 AA.
AC W17968;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Nle31]hPTH(1-34)NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 31 /label= Nle
FT modified_site 31 /label= Nle
FT modified_site 34 /note= "In amide form"
FT FT
FN W09702834-AA.
PD 30-JAN-1997.
PF 03-JUL-1996: U11292.
PR 13-JUL-1995: US-001105.
PR 06-SEP-1995: US-003305.
PR 29-MAR-1996: US-626186.
PA (BIOM-) BIOMEASURE INC.
PI Dong ZX;
DR WPI: 97-118819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which
PT stimulate bone growth and are used for treatment of osteoporosis and
PT bone fracture
PS Claim 20: Page -: 33pp: English.
CC The present sequence is a specific example of a human parathyroid
CC hormone (hPTH) analogue from fragment 1-34 in which at least the amino
CC acid residue at position 1 is alpha, beta-diaminopropionic acid,
CC the amino acid residue at position 27 is homocysteine, or the amino acid
CC residue at position 31 is norleucine. In this example the Val residue at
CC position 31 in the wild-type has been substituted by Nle. The hPTH
CC analogues stimulate bone growth and so are useful in human or
CC veterinary medicine for treatment of osteoporosis and bone fracture,
CC optionally in conjunction with anti-resorptive therapy (bisphosphonates
CC and calcitonin).
CC N.B. The present sequence does not appear in the specification. It
CC corresponds to the known hPTH 1-34 fragment with the modifications
CC as stated in the claim.
SQ Sequence 34 AA;
Query Match 100.0%; Score 44; DB 22; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.47e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 khlnsm 18
| | | | |
QY 1 KHLNSM 6

RESULT 2

ID W17939 standard; peptide; 34 AA.
AC W17939;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
OS bone fracture.
OS Homo sapiens.
OS Synthetic.

FH Key Location/Qualifiers
FT modified_site 7 /label= OTHER

FT modified_site 11 /note= "Cyclohexylalanine (Cha)"
FT /label= OTHER
FT /note= "Cha"

FT modified_site 34 /note= "in amide form"

PN W09702834-A1.
PD 30-JAN-1997.

PF 03-JUL-1996; U11292.

PR 13-JUL-1995; US-001105.

PR 06-SEP-1995; US-003305.

PR 29-MAR-1996; US-626186.

PA (BIOM-) BIOMESURE INC.

PI Dong ZX.

PI MPI; 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which

PT stimulate bone growth and are used for treatment of osteoporosis and

PT bone fracture

PS Claim 5; Page -: 33pp; English.

CC The present sequence is a specific example of a human parathyroid

CC hormone (hPTH) analogue from fragment 1-34 in which at least one

CC of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31

CC is cyclohexylalanine (Cha). In this example the leu residue at

CC position 7 and the leu at position 11 in the wild-type have been

CC substituted by Cha. The hPTH analogues stimulate bone growth and so

CC are useful in human or veterinary medicine for treatment of

CC osteoporosis and bone fracture, optionally in conjunction with

CC anti-resorptive therapy (bisphosphonates and calcitonin).

CC N.B. The present sequence does not appear in the specification. It

CC corresponds to the known hPTH 1-34 fragment with the modifications

CC as stated in the claim.

SC Sequence 34 AA;

Query Match 100.0%; Score 44; DB 22; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.47e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 khlnsm 18
| | | | |
QY 1 KHLNSM 6

Search completed: Thu Jul 30 10:22:35 1998
Job time : 13 secs.

W D S E I F
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:21:36 1998; Maspar time 3.04 Seconds
Tabular output not generated. 72.203 Million cell updates/sec

Title: >US-08-817-547A-11
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 KHLNSM 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 18.883; Variance 20.866; scale 0.505

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	44	100.0	34	5	12WA parathyroid hormone (2.07e+00	
2	44	100.0	34	5	12WE parathyroid hormone (2.07e+00	
3	44	100.0	34	5	12WG parathyroid hormone 4 2.07e+00	
4	44	100.0	34	5	12WF parathyroid hormone 4 2.07e+00	
5	44	100.0	35	5	12WD parathyroid hormone (2.07e+00	
6	44	100.0	36	5	12WB parathyroid hormone (2.07e+00	
7	44	100.0	37	5	12WB parathyroid hormone (2.07e+00	
8	44	100.0	115	1	PTHU parathyroid hormone P 2.07e+00	
9	44	100.0	2105	1	RNA-directed RNA poly 2.07e+00	
10	41	93.2	3005	2	homeotic protein zfh- 1.77e+01	
11	40	90.9	37	5	12WC parathyroid hormone (1.77e+01	
12	40	90.9	115	2	JC4202 parathyroid hormone - 1.77e+01	
13	40	90.9	115	1	PTBO parathyroid hormone P 1.77e+01	
14	40	90.9	421	2	D69981 conserved hypothetical 2.97e+01	
15	39	88.6	662	2	S61193 probable membrane pro 4.93e+01	
16	38	86.4	545	2	E69907 DNA recombinase homol 8.09e+01	
17	37	84.1	193	2	E69469 hypothetical protein 8.09e+01	
18	37	84.1	196	2	C69839 phospho-adenylyl sulf 8.09e+01	
19	37	84.1	208	2	D65041 hypothetical protein 8.09e+01	
20	37	84.1	247	2	S72904 phosphoglycerate muta 8.09e+01	
21	37	84.1	253	1	PMHUYM phosphoglycerate muta 8.09e+01	
22	37	84.1	253	1	PMRTYM phosphoglycerate muta 8.09e+01	
23	37	84.1	271	2	S67072 probable membrane pro 8.09e+01	

24	37	84.1	295	5	2AT2A	Aspartate transcarbam 8.09e+01
25	37	84.1 <td>295<td>5<th>2AT2B</th><th>Aspartate transcarbam 8.09e+01</th></td></td>	295 <td>5<th>2AT2B</th><th>Aspartate transcarbam 8.09e+01</th></td>	5 <th>2AT2B</th> <th>Aspartate transcarbam 8.09e+01</th>	2AT2B	Aspartate transcarbam 8.09e+01
26	37	84.1 <td>304<td>5<th>2AT2C</th><th>Aspartate transcarbam 8.09e+01</th></td></td>	304 <td>5<th>2AT2C</th><th>Aspartate transcarbam 8.09e+01</th></td>	5 <th>2AT2C</th> <th>Aspartate transcarbam 8.09e+01</th>	2AT2C	Aspartate transcarbam 8.09e+01
27	37	84.1 <td>295<td>1<th>OWBSAC</th><th>aspartate carbamoyl tr 8.09e+01</th></td></td>	295 <td>1<th>OWBSAC</th><th>aspartate carbamoyl tr 8.09e+01</th></td>	1 <th>OWBSAC</th> <th>aspartate carbamoyl tr 8.09e+01</th>	OWBSAC	aspartate carbamoyl tr 8.09e+01
28	37	84.1 <td>3429<td>8</td><th>glycerol-3-phosphate d 8.09e+01</th><th></th></td>	3429 <td>8</td> <th>glycerol-3-phosphate d 8.09e+01</th> <th></th>	8	glycerol-3-phosphate d 8.09e+01	
29	37	84.1 <td>430<td>2<th>A65165</th><th>protein dfr - Escheri 8.09e+01</th></td></td>	430 <td>2<th>A65165</th><th>protein dfr - Escheri 8.09e+01</th></td>	2 <th>A65165</th> <th>protein dfr - Escheri 8.09e+01</th>	A65165	protein dfr - Escheri 8.09e+01
30	37	84.1 <td>438<td>2<th>A64147</th><th>hypothetical protein 8.09e+01</th></td></td>	438 <td>2<th>A64147</th><th>hypothetical protein 8.09e+01</th></td>	2 <th>A64147</th> <th>hypothetical protein 8.09e+01</th>	A64147	hypothetical protein 8.09e+01
31	37	84.1 <td>491<td>2<th>I40990</th><th>signal transducer amp 8.09e+01</th></td></td>	491 <td>2<th>I40990</th><th>signal transducer amp 8.09e+01</th></td>	2 <th>I40990</th> <th>signal transducer amp 8.09e+01</th>	I40990	signal transducer amp 8.09e+01
32	37	84.1 <td>491<td>2<th>I40991</th><th>signal transducer amp 8.09e+01</th></td></td>	491 <td>2<th>I40991</th><th>signal transducer amp 8.09e+01</th></td>	2 <th>I40991</th> <th>signal transducer amp 8.09e+01</th>	I40991	signal transducer amp 8.09e+01
33	37	84.1 <td>491<td>2<th>I40989</th><th>signal transducer amp 8.09e+01</th></td></td>	491 <td>2<th>I40989</th><th>signal transducer amp 8.09e+01</th></td>	2 <th>I40989</th> <th>signal transducer amp 8.09e+01</th>	I40989	signal transducer amp 8.09e+01
34	37	84.1 <td>491<td>2<th>S37391</th><th>amg protein - Escher 8.09e+01</th></td></td>	491 <td>2<th>S37391</th><th>amg protein - Escher 8.09e+01</th></td>	2 <th>S37391</th> <th>amg protein - Escher 8.09e+01</th>	S37391	amg protein - Escher 8.09e+01
35	37	84.1 <td>585<td>2<th>C36858</th><th>G3P protein - variola 8.09e+01</th></td></td>	585 <td>2<th>C36858</th><th>G3P protein - variola 8.09e+01</th></td>	2 <th>C36858</th> <th>G3P protein - variola 8.09e+01</th>	C36858	G3P protein - variola 8.09e+01
36	37	84.1 <td>648<td>1<th>NPVZCP</th><th>nucleoside-triphospha 8.09e+01</th></td></td>	648 <td>1<th>NPVZCP</th><th>nucleoside-triphospha 8.09e+01</th></td>	1 <th>NPVZCP</th> <th>nucleoside-triphospha 8.09e+01</th>	NPVZCP	nucleoside-triphospha 8.09e+01
37	37	84.1 <td>648<td>1<th>NPVZAM</th><th>nucleoside-triphospha 8.09e+01</th></td></td>	648 <td>1<th>NPVZAM</th><th>nucleoside-triphospha 8.09e+01</th></td>	1 <th>NPVZAM</th> <th>nucleoside-triphospha 8.09e+01</th>	NPVZAM	nucleoside-triphospha 8.09e+01
38	37	84.1 <td>700<td>2<th>S12053</th><th>protein-tyrosine-phos 8.09e+01</th></td></td>	700 <td>2<th>S12053</th><th>protein-tyrosine-phos 8.09e+01</th></td>	2 <th>S12053</th> <th>protein-tyrosine-phos 8.09e+01</th>	S12053	protein-tyrosine-phos 8.09e+01
39	37	84.1 <td>931<td>2<th>G69615</th><th>Arp-dependent DNA hel 8.09e+01</th></td></td>	931 <td>2<th>G69615</th><th>Arp-dependent DNA hel 8.09e+01</th></td>	2 <th>G69615</th> <th>Arp-dependent DNA hel 8.09e+01</th>	G69615	Arp-dependent DNA hel 8.09e+01
40	37	84.1 <td>1101<td>2<th>S51823</th><th>myosin heavy chain AT 8.09e+01</th></td></td>	1101 <td>2<th>S51823</th><th>myosin heavy chain AT 8.09e+01</th></td>	2 <th>S51823</th> <th>myosin heavy chain AT 8.09e+01</th>	S51823	myosin heavy chain AT 8.09e+01
41	36	81.8 <td>101<td>2<th>S64056</th><th>probable membrane pro 1.32e+02</th></td></td>	101 <td>2<th>S64056</th><th>probable membrane pro 1.32e+02</th></td>	2 <th>S64056</th> <th>probable membrane pro 1.32e+02</th>	S64056	probable membrane pro 1.32e+02
42	36	81.8 <td>142<td>2<th>S04071</th><th>hemoglobin alpha chal 1.32e+02</th></td></td>	142 <td>2<th>S04071</th><th>hemoglobin alpha chal 1.32e+02</th></td>	2 <th>S04071</th> <th>hemoglobin alpha chal 1.32e+02</th>	S04071	hemoglobin alpha chal 1.32e+02
43	36	81.8 <td>511<td>2<th>JC1404</th><th>CD81-box DNA-binding 1.32e+02</th></td></td>	511 <td>2<th>JC1404</th><th>CD81-box DNA-binding 1.32e+02</th></td>	2 <th>JC1404</th> <th>CD81-box DNA-binding 1.32e+02</th>	JC1404	CD81-box DNA-binding 1.32e+02
44	36	81.8 <td>587<td>2<th>H64045</th><th>msbA protein - Haemop 1.32e+02</th></td></td>	587 <td>2<th>H64045</th><th>msbA protein - Haemop 1.32e+02</th></td>	2 <th>H64045</th> <th>msbA protein - Haemop 1.32e+02</th>	H64045	msbA protein - Haemop 1.32e+02
45	36	81.8 <td>922<td>2<th>S31164</th><th>Arp-dependent ClpB pr 1.32e+02</th></td></td>	922 <td>2<th>S31164</th><th>Arp-dependent ClpB pr 1.32e+02</th></td>	2 <th>S31164</th> <th>Arp-dependent ClpB pr 1.32e+02</th>	S31164	Arp-dependent ClpB pr 1.32e+02

ALIGNMENTS

RESULT	1	12WA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		PTH(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		TN001717	
REFERENCE		TN001717	
#authors		Marx, U.C.	
#book		in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	
KEYWORDS		hormone	
FEATURE			
6-9		#region helix (right hand alpha)\	
19-30		#region helix (right hand alpha)	
SUMMARY		#length 34 #molecular-weight 4118 #checksum 5629	
Query Match		100.0%; Score 44; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 2.07e+00;	
Matches		6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	13 KHLNSM 18		
Oy	1 KHLNSM 6		
RESULT	2	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		PTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		TN001721	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15-25
 SUMMARY #region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 44; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.07e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 KHLNSM 15
 QY 1 KHLNSM 6

Search completed: Thu Jul 30 10:22:04 1998
 Job time : 28 secs.

RP REVISIONS.
 RX MEDLINE; 75146516.
 RA KEUTMANN H.T., NIALI H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 75059220.
 RA TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALI H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 73227467.
 RA ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA KINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 93345518.
 RA BARDEEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE; 95318084.
 RA MARK U.C., AUSTERMANN S., BAYER P., ADERMAN K., EICHAUT A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE; 91009811.
 RA ANNOUD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (PTH).
 CC EMBL; U00301; G190704; -.
 DR EMBL; V00597; G37144; -.
 DR EMBL; A29146; E186700; -.
 DR PIR; A01536; PTHU.
 DR PIR; A19339; A19339.
 DR PDB; 1HRH; 10-JUL-95.
 DR PDB; 1HTH; 15-OCT-97.
 DR PDB; 1ZWA; 12-MAR-97.
 DR PDB; 1ZWB; 12-MAR-97.
 DR PDB; 1ZWC; 12-MAR-97.
 DR PDB; 1ZWD; 12-MAR-97.
 DR PDB; 1ZWE; 12-MAR-97.
 DR PDB; 1ZNF; 16-JUN-97.
 DR PDB; 1ZNG; 16-JUN-97.
 DR MIM; 146200; -.
 DR MIM; 168450; -.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA; 12861 MW; 243E87C7 CRC32;
 N -> D (IN REF. 5).
 PARATHYROID HORMONE.
 C -> R (IN FTH: LEADS TO INEFFICIENT
 PROCESSING OF THE PRECURSOR).
 Query Match 100.0%; Score 44; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 3.21e-01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 KHLNSM 49
 |||||
 QY 1 KHLNSM 6
 RESULT 2
 ID POLR_ASGVP STANDARD; PRT; 2105 AA.
 AC P36309;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE GENOME POLYPROTEIN (CONTAINS: RNA REPLICASE (EC 2.7.7.48); HELICASE;
 DE COAT PROTEIN).
 OS APPLE STEM GROOVING VIRUS (STRAIN P-209) (ASGV).
 OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CAPILLOVIRIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93033164.
 RA YOSHIKAWA N., SASAKI E., KATO M., TAKAHASHI T.;
 RL VIROLOGY 191:98-105(1992).
 CC -1- PTM: THE N-TERMINAL OF THE COAT PROTEIN IS BLOCKED.
 CC -1- THE COAT PROTEIN IS LOCATED IN THE CARBOXY-TERMINAL REGION OF
 CC THIS POLYPROTEIN.
 DR EMBL; D14995; G285608; -.
 DR PIR; A44059; A44059.
 KW RNA-DIRECTED RNA POLYMERASE; POLYPROTEIN; ATP-BINDING; COAT PROTEIN;
 KW HELICASE.
 FT NP_BIND 781 788
 FT DOMAIN 1364 1453
 FT SEQUENCE 2105 AA; 241240 MW; B3EE0CC2C CRC32;
 ATP (POTENTIAL).
 POLYMERASE ACTIVE SITE.
 Query Match 100.0%; Score 44; DB 1; Length 2105;
 Best Local Similarity 100.0%; Pred. No. 3.21e-01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: Thu Jul 30 10:20:44 1998
 Job time : 7 secs.

DT 01-JAN-1998 (TREMERE). 05, LAST ANNOTATION UPDATE)
 DE ZINC FINGER HOMEODOMAIN PROTEIN (3' PARTIAL) (FRAGMENT).
 GN A-418G10.1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ADAMS M.D., LOFTUS B.J., ZHOU L., LABONARD M., FUHRMAN J.,
 RA BRANDON R., KIM U.J., KERLAVAGE A.R., VENTER J.C.;
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AC002044; G2347080; -
 KM HOMEODOMAIN; DNA-BINDING; NUCLEAR PROTEIN.
 FT NON_TER 1072 1072
 SQ SEQUENCE 1072 AA; 115896 MW; 78611913 CRC32;

Query Match
 Best Local Similarity 93.2%; Score 41; DB 2; Length 1072;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 749 KHLNNM 754
 1 KHLNSM 6

Search completed: Thu Jul 30 10:21:19 1998
 Job time : 18 secs.

Db 8 hlasm 12
 |||||
 QY 1 HLNSM 5

RESULT 2

ID P40427 standard; peptide; 32 AA.
 AC P40427;
 DT 22-JUL-1992 (first entry)
 DE Parathyroid antagonist peptide.
 KW Human thyroid hormone.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 32 /note= "Phe or Tyr"
 FT J59042351-A.
 PN 08-MAR-1984.
 PF 1-SEP-1982; 150702.
 (TOXN) TOYO JOZO KK.
 WPI; 84-097433/16.
 h-PTH Peptide (3-34) derivatives - are N-terminal fragments of human
 thyroid hormone
 PT Claim 1, Page 1; 25pp; Japanese.
 PS The peptide is an N-terminal fragment deriv. of human thyroid
 CC hormone (amino acids 3-34) and is an antagonist of parathyroid
 CC hormone. It is expected to be a therapeutic agent of hyperfunction
 CC of accessory thyroid.
 SQ Sequence 32 AA;

Query Match 100.0%; Score 37; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.89e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 12 hlasm 16
 |||||
 QY 1 HLNSM 5

Search completed: Thu Jul 30 10:24:56 1998
 Job time : 11 secs.

W D S E L I F (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:24:01 1998; Maspar time 3.08 Seconds
Tabular output not generated. 59.270 Million cell updates/sec

Title: >US-08-817-547A-12
Description: (1-5) from US08817547A.pep
Perfect Score: 37
Sequence: 1 HLNSM 5

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 17.600; Variance 17.971; scale 0.979

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	37	100.0	34	5 1ZWA	parathyroid hormone (1.96e+01	
2	37	100.0	34	5 1ZWE	parathyroid hormone (1.96e+01	
3	37	100.0	34	5 1ZMG	parathyroid hormone (1.96e+01	
4	37	100.0	34	5 1ZWF	parathyroid hormone (1.96e+01	
5	37	100.0	35	5 1ZWD	parathyroid hormone (1.96e+01	
6	37	100.0	36	5 1ZWB	parathyroid hormone (1.96e+01	
7	37	100.0	37	5 1HPH	parathyroid hormone (1.96e+01	
8	37	100.0	115	1 PTHU	parathyroid hormone (1.96e+01	
9	37	100.0	193	2 E69469	hypothetical protein	1.96e+01
10	37	100.0	208	2 D65041	hypothetical protein	1.96e+01
11	37	100.0	384	2 S73429	glycerol-3-phosphate d	1.96e+01
12	37	100.0	585	2 C36858	G3R protein - variola	1.96e+01
13	37	100.0	2105	1 A44059	RNA-directed RNA poly	1.96e+01
14	35	94.6	186	2 H64785	hypothetical protein	5.87e+01
15	35	94.6	216	2 C64622	osmoprotection protei	5.87e+01
16	35	94.6	369	2 S74983	hypothetical protein	5.87e+01
17	35	94.6	389	2 UCS136	naringenin-chalcone s	5.87e+01
18	35	94.6	396	2 S20515	naringenin-chalcone s	5.87e+01
19	35	94.6	398	2 S58190	naringenin-chalcone s	5.87e+01
20	35	94.6	410	2 S12224	naringenin-chalcone s	5.87e+01
21	35	94.6	419	2 S74500	zeaxanthin glucosyl t	5.87e+01
22	35	94.6	423	2 T64063	histidine--tRNA ligas	5.87e+01
23	35	94.6	500	2 S50508	ANP1 protein - yeast	5.87e+01

24	35	94.6	587	2	S61038	D-lactate dehydrogena	5.87e+01
25 <td>35</td> <td>94.6</td> <td>662</td> <td>2</td> <td>S61193</td> <th>probable membrane pro</th> <th>5.87e+01</th>	35	94.6	662	2	S61193	probable membrane pro	5.87e+01
26 <td>35</td> <td>94.6</td> <td>684</td> <td>2</td> <td>B69308</td> <th>conserved hypotheticala</th> <th>5.87e+01</th>	35	94.6	684	2	B69308	conserved hypotheticala	5.87e+01
27 <td>35</td> <td>94.6</td> <td>696</td> <td>2</td> <td>A65130</td> <th>hypothetical 79.5 kd</th> <th>5.87e+01</th>	35	94.6	696	2	A65130	hypothetical 79.5 kd	5.87e+01
28 <td>35</td> <td>94.6</td> <td>880</td> <td>2</td> <td>S49627</td> <th>regulatory protein AR</th> <th>5.87e+01</th>	35	94.6	880	2	S49627	regulatory protein AR	5.87e+01
29 <td>35</td> <td>94.6</td> <td>922</td> <td>2</td> <td>S31164</td> <th>AMP-dependent ClPB pr</th> <th>5.87e+01</th>	35	94.6	922	2	S31164	AMP-dependent ClPB pr	5.87e+01
30 <td>35</td> <td>94.6</td> <td>1642</td> <td>2</td> <td>151018</td> <th>cobra venom factor pr</th> <th>5.87e+01</th>	35	94.6	1642	2	151018	cobra venom factor pr	5.87e+01
31 <td>35</td> <td>94.6</td> <td>3411</td> <td>1</td> <td>GNMVP</td> <th>genome polypoteins -</th> <th>5.87e+01</th>	35	94.6	3411	1	GNMVP	genome polypoteins -	5.87e+01
32 <td>35</td> <td>94.6</td> <td>151</td> <td>2</td> <td>F69986</td> <th>acetyltransferase hom</th> <th>9.99e+01</th>	35	94.6	151	2	F69986	acetyltransferase hom	9.99e+01
33 <td>34</td> <td>91.9</td> <td>154</td> <td>2</td> <td>J00860</td> <th>hypothetical 18k prot</th> <th>9.99e+01</th>	34	91.9	154	2	J00860	hypothetical 18k prot	9.99e+01
34 <td>34</td> <td>91.9</td> <td>232</td> <td>2</td> <td>S72439</td> <th>GTP cyclonhydrolase I</th> <th>9.99e+01</th>	34	91.9	232	2	S72439	GTP cyclonhydrolase I	9.99e+01
35 <td>34</td> <td>91.9</td> <td>317</td> <td>2</td> <td>152575</td> <th>gene NRK protein - mo</th> <th>9.99e+01</th>	34	91.9	317	2	152575	gene NRK protein - mo	9.99e+01
36 <td>34</td> <td>91.9</td> <td>346</td> <td>2</td> <td>S62197</td> <th>molymbdenum formylmeth</th> <th>9.99e+01</th>	34	91.9	346	2	S62197	molymbdenum formylmeth	9.99e+01
37 <td>34</td> <td>91.9</td> <td>354</td> <td>2</td> <td>JC1366</td> <th>tyrosine kinase recep</th> <th>9.99e+01</th>	34	91.9	354	2	JC1366	tyrosine kinase recep	9.99e+01
38 <td>34</td> <td>91.9</td> <td>396</td> <td>1</td> <td>R3BYM1</td> <th>ribosomal protein var</th> <th>9.99e+01</th>	34	91.9	396	1	R3BYM1	ribosomal protein var	9.99e+01
39 <td>34</td> <td>91.9</td> <td>447</td> <td>2</td> <td>C64828</td> <th>hypothetical protein</th> <th>9.99e+01</th>	34	91.9	447	2	C64828	hypothetical protein	9.99e+01
40 <td>34</td> <td>91.9</td> <td>593</td> <td>2</td> <td>A47186</td> <th>receptor protein tyro</th> <th>9.99e+01</th>	34	91.9	593	2	A47186	receptor protein tyro	9.99e+01
41 <td>34</td> <td>91.9</td> <td>594</td> <td>2</td> <td>156248</td> <th>receptor tyrosine kin</th> <th>9.99e+01</th>	34	91.9	594	2	156248	receptor tyrosine kin	9.99e+01
42 <td>34</td> <td>91.9</td> <td>594</td> <td>2</td> <td>158386</td> <th>receptor tyrosine kin</th> <th>9.99e+01</th>	34	91.9	594	2	158386	receptor tyrosine kin	9.99e+01
43 <td>34</td> <td>91.9</td> <td>607</td> <td>2</td> <td>137560</td> <th>protein-tyrosine kin</th> <th>9.99e+01</th>	34	91.9	607	2	137560	protein-tyrosine kin	9.99e+01
44 <td>34</td> <td>91.9</td> <td>3005</td> <td>2</td> <td>S33642</td> <th>homeotic protein zfh-</th> <th>9.99e+01</th>	34	91.9	3005	2	S33642	homeotic protein zfh-	9.99e+01

ALIGNMENTS

RESULT	1	1ZWA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		HPTH(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		TN001717	
REFERENCE		TN001717	
#authors		Marx, U.C.	
#book		in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	
KEYWORDS		hormone	
FEATURE			
6-9		#region helix (right hand alpha)\	
19-30		#region helix (right hand alpha)	
SUMMARY		#length 34 #molecular-weight 4118 #checksum 5629	
Query Match		100.0%; Score 37; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.96e+01;	
Matches		5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	14	HLNSM 18	
QY	1	HLNSM 5	
RESULT	2	1ZWE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:1ZWE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15-25 #region helix (right hand alpha)
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 37; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.96e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

DB 11 HLNSM 15
 QY 1 HLNSM 5

Search completed: Thu Jul 30 10:24:27 1998
 Job time : 26 secs.

WIDEORBIT (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:22:54 1998; Maspar time 2.01 Seconds
62.468 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-12
Description: (1-5) from US08817547A.pep
Perfect Score: 37
Sequence: 1 HLNSM 5

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 18.404; Variance 15.219; scale 1.209

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	37	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	5.14e+00
2	37	100.0	208	1	YFJY_ECOLI HYPOTHETICAL 24.6 KD P	5.14e+00
3	37	100.0	384	1	Y039_MYCPN HYPOTHETICAL PROTEIN M	5.14e+00
4	37	100.0	692	1	YI13_CAEEL PROBABLE G. PROTEIN-COU	5.14e+00
5	37	100.0	2105	1	POLR_ASGVP GENOME POLYPROTEIN (CN	5.14e+00
6	35	94.6	389	1	CHS2_LYCES CHALCONE SYNTHASE 2 (E	1.85e+01
7	35	94.6	396	1	CHSY_PINSY CHALCONE SYNTHASE (EC	1.85e+01
8	35	94.6	398	1	CHSY_ORYSA CHALCONE SYNTHASE (EC	1.85e+01
9	35	94.6	422	1	SYH_HABIN HISTIDYL-TRNA SYNTHETA	1.85e+01
10	35	94.6	500	1	ANPL_YEAST AMINONITROPHENYL PROPA	1.85e+01
11	35	94.6	587	1	DLDI_YEAST D-LACTATE DEHYDROGENAS	1.85e+01
12	35	94.6	662	1	PMT7_YEAST DOLICHYL-PHOSPHATE-MAN	1.85e+01
13	35	94.6	696	1	YHFK_ECOLI HYPOTHETICAL 79.5 KD P	1.85e+01
14	35	94.6	859	1	Y0D3_CAEEL HYPOTHETICAL 96.7 KD P	1.85e+01
15	35	94.6	880	1	ARG2_YEAST ARGININE METABOLISM RE	1.85e+01
16	35	94.6	922	1	CLPA_PRAA ATP-DEPENDENT CLP PROT	1.85e+01
17	35	94.6	3411	1	POLG_YEFAV GENOME POLYPROTEIN (CO	1.85e+01
18	35	94.6	3411	1	POLG_YEFAV GENOME POLYPROTEIN (CO	1.85e+01
19	34	91.9	154	1	YRTE_ECOLI HYPOTHETICAL 18.0 KD P	3.44e+01
20	34	91.9	341	1	YK84_CAEEL HYPOTHETICAL 28.1 KD P	3.44e+01
21	34	91.9	339	1	RMAR_CANGA MITOCHONDRIAL RIBOSOM	3.44e+01
22	34	91.9	355	1	DYR1_BRARE DYR-1 PROTEIN PRECURSO	3.44e+01
23	34	91.9	396	1	RMAR_YEAST MITOCHONDRIAL RIBOSOM	3.44e+01

RESULT	ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	21-JUL-1986	(REL. 01, CREATED)				
DT	13-AUG-1987	(REL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;					
OC	EUTHERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 82150870.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.;					
RA	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RX	MEDLINE; 74174967.					
RA	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RX	MEDLINE; 7411656.					
RA	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;					
RA	O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T. JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RX	MEDLINE; 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;					
RA	POTTS J.T. JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;					
RA	O'RIORDAN J.L.H., POTTS J.T. JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.;					
RL	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGGAR G.W., VAN RIENSCHOTEN J., GREEN E., NIALL H.D.,
 RL KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MALER R.,
 RL KINIGER B., RITTEL W., SIEBER P.;
 RN [10]
 RP HELV. CHIM. ACTA 56:470-473(1973).
 RX STRUCTURE BY NMR OF 32-65.
 RA MEDLINE: 91298748.
 RL KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RN [11]
 RP BIOCHEMISTRY 30:6936-6942(1991).
 RX STRUCTURE BY NMR OF 32-65.
 RA MEDLINE: 93345518.
 RL BARDEN J.A., CUTHBERTSON R.M.;
 RN [12]
 RP EUR. J. BIOCHEM. 215:315-321(1993).
 RX STRUCTURE BY NMR OF 32-68.
 RA MEDLINE: 95318084.
 RL MARX U.C., AUSTERMANN S., BAYER P., ADERHANN K., ECHART A.,
 RA STIGT H., WALTER S., SCHMID F.-X., JABENICKE R., FORSMANN W.-G.,
 RL KOSCH P.;
 RN [13]
 RP J. BIOL. CHEM. 270:15194-15202(1995).
 RX VARIANT ARG-18.
 RA MEDLINE: 91009811.
 RL ARNOOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RN KRONENBERG H.M.;
 CC J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 DR EMBL: J00301; G180704; -.
 DR EMBL: V00597; G37144; -.
 DR EMBL: A29146; E186700; -.
 DR PIR: A01536; PTHU.
 DR PIR: A19339; A19339.
 DR PDB: 1HPH; 10-JUL-95.
 DR PDB: 1HTH; 15-OCT-97.
 DR PDB: 12WA; 12-MAR-97.
 DR PDB: 12WB; 12-MAR-97.
 DR PDB: 12WC; 12-MAR-97.
 DR PDB: 12WD; 12-MAR-97.
 DR PDB: 12WE; 12-MAR-97.
 DR PDB: 12WF; 16-JUN-97.
 DR PDB: 12WG; 16-JUN-97.
 DR PDB: 12WG; 16-JUN-97.
 DR MIM: 146200; -.
 DR MIM: 168450; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 23
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107 PARATHYROID HORMONE.
 FT SEQUENCE 115 AA; 12861 MM; 24388/C7 CRC32; C -> R (IN FTH; LEADS TO INEFFECTIVE
 N -> D (IN REF. 5)).
 Query Match 100.0%; Score 37; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 5.14e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 45 HLNSM 49
 QY 1 HLNSM 5
 RESULT 2
 ID YFJU_ECOLI STANDARD; PRT; 208 AA.
 AC P52125;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 GN HYPOTHETICAL 24.6 KD PROTEIN IN ALPA-GABD INTERGENIC REGION (0208).
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RA BRATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: STRONG, TO E.COLI YAKG.
 DR EMBL: U36840; G1033121; -.
 DR EMBL: AE000348; G1768979; -.
 DR ECOGENE: EGI3196; YFJU.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 208 AA; 24560 MM; B33D5203 CRC32;
 Query Match 100.0%; Score 37; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.14e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 29 HLNSM 33
 QY 1 HLNSM 5

Search completed: Thu Jul 30 10:23:01 1998
 Job time : 7 secs.

RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBECK R.,
RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T., COTTON M.D.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RM (2)
RP SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A.,
RA DODSON R.J., GRINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L.,
RA KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D.,
RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBECK R.,
RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T., COTTON M.D.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL, AEO00981, G2648792; -
KM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 193 AA; 22041 MW; 59F1ED0E CRC32;

Query Match 100.0%; Score 37; DB 9; Length 193;
Best local Similarity 100.0%; Pred. No. 6.33e+00;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 44 HLNSM 48
QY 1 HLNSM 5

Search completed: Thu Jul 30 10:23:44 1998
Job time : 26 secs.

WIDEOR (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:27:11 1998; MasPar time 2.64 Seconds
52.320 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-13
Description: (1-9) from US08817547A.pep
Perfect Score: 62
Sequence: 1 HNLGKHLNS 9

Scoring table:
PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.334; Variance 52.987; scale 0.289

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	62	100.0	34	9	R58181 [Thr33, Ala34]-hPTH(1-36)-NH2	4.68e+00
2	62	100.0	34	22	W17957 Human parathyroid hor	4.68e+00
3	62	100.0	34	22	W17954 Human parathyroid hor	4.68e+00
4	62	100.0	34	22	W17955 Human parathyroid hor	4.68e+00
5	62	100.0	34	22	W17950 Human PTH analogue [C	4.68e+00
6	62	100.0	34	22	W17969 Human parathyroid hor	4.68e+00
7	62	100.0	34	22	W17970 Human PTH analogue [D	4.68e+00
8	62	100.0	34	7	R34354 Human parathyroid hor	4.68e+00
9	62	100.0	34	7	R34353 Human parathyroid hor	4.68e+00
10	62	100.0	34	22	W17943 Human parathyroid hor	4.68e+00
11	62	100.0	34	22	W17949 Human parathyroid hor	4.68e+00
12	62	100.0	34	22	W17948 Human parathyroid hor	4.68e+00
13	62	100.0	35	14	R74516 Parathyroid hormone p	4.68e+00
14	62	100.0	35	14	R74517 Parathyroid hormone p	4.68e+00
15	62	100.0	35	14	R74402 Parathyroid hormone p	4.68e+00
16	62	100.0	35	14	R74401 Parathyroid hormone p	4.68e+00
17	62	100.0	35	14	R74429 Parathyroid hormone p	4.68e+00
18	62	100.0	35	14	R74431 Parathyroid hormone p	4.68e+00
19	62	100.0	36	9	R58182 [Nval]-hPTH(1-36)-NH2	4.68e+00

20	62	100.0	36	9	R58279 [Lys20]-hPTH(1-36)-NH	4.68e+00
21	62	100.0	36	9	R58177 [Methionine-2-carboxy	4.68e+00
22	62	100.0	36	9	R58176 [Hexahydroxyindazole-	4.68e+00
23	62	100.0	36	9	R58248 N-Dimethyl-1-[Ala1]-hPT	4.68e+00
24	62	100.0	36	9	R58247 [Hyp1]-hPTH(1-36)-NH2	4.68e+00
25	62	100.0	36	2	R23995 Human parathyroid hor	4.68e+00
26	62	100.0	36	9	R58246 Acetyl-hPTH(1-36)-NH2	4.68e+00
27	62	100.0	36	9	R58242 [Lys(isopropyl)13]-hP	4.68e+00
28	62	100.0	36	9	R58175 [Pyridine-2-carboxyl1	4.68e+00
29	62	100.0	38	9	R58295 [D-Val35]-hPTH(1-36)-	4.68e+00
30	62	100.0	38	9	R58164 [Asp33]-hPTH(1-38)-OH	4.68e+00
31	62	100.0	44	26	P30015 Human parathyroid hor	4.68e+00
32	62	100.0	47	25	W21945 Fusion protein compri	4.68e+00
33	62	100.0	84	27	W25687 Human parathyroid hor	4.68e+00
34	62	100.0	84	4	R21198 Human parathyroid hor	4.68e+00
35	62	100.0	84	4	R21199 Human parathyroid hor	4.68e+00
36	62	100.0	84	4	W29420 Human parathyroid hor	4.68e+00
37	62	100.0	84	4	R21153 Human parathyroid hor	4.68e+00
38	62	100.0	84	4	R21152 Human parathyroid hor	4.68e+00
39	62	100.0	84	6	R30851 Generic human parathy	4.68e+00
40	62	100.0	84	7	R34460 Human parathyroid hor	4.68e+00
41	62	100.0	84	4	R21250 Human parathyroid hor	4.68e+00
42	62	100.0	84	4	R21251 Human parathyroid hor	4.68e+00
43	62	100.0	84	4	R23245 Human parathyroid hor	4.68e+00
44	62	100.0	84	4	R21243 Human parathyroid hor	4.68e+00
45	62	100.0	229	9	R47971 Sequence of a full-le	4.68e+00

ALIGNMENTS

RESULT 1
ID R58181 standard; peptide; 34 AA.
AC R58181;
DT 20-SEP-1994 (first entry)
DE [Thr33, Ala34]-hPTH(1-34)-NH2.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 34 /note="in amide form"
FT
PN GB269176-A.
PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PF 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gilbert F, Gram H, Lewis I, Ramage P, Schneider H,
PI Maelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 179; Page 43; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 34 AA:
Query Match 100.0%; Score 62; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.68e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhlns 17
 |||||
 QY 1 HNLGKHLNS 9

RESULT 2

ID W17957 standard; peptide: 34 AA.
 AC W17957;
 DT 29-JUL-1997 (first entry)
 DE Human parathyroid hormone analogue [Alb3]hPTH(1-34)NH2.
 KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 OS bone fracture.
 OS Homo sapiens.
 OS Synthetic.
 FH Key
 FT modified_site 3 Location/Qualifiers
 FT modified_site 34 /label= Alb

modified_site 34 /note= "In amide form"

PD WO9702834-A1.
 PE 30-JAN-1997.
 PR 03-JUL-1996; U11292.
 PR 13-JUL-1995; US-001105.
 PR 06-SEP-1995; US-003305.
 PR 29-MAR-1996; US-626186.
 PA (BIOM-) BIOMEASURE INC.
 PI Dong ZX;

DR WPI: 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture

PS Claim 11; Page -: 33pp; English.

CC The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 is alpha-aminoisobutyric acid (Aib). In this example the Ser residue at position 3 of the wild-type has been substituted by Aib. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).
 CC N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim.
 CC as stated in the claim.
 SQ Sequence 34 AA;

Query Match

100.0%; Score 62; DB 22; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.66e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhlns 17
 |||||
 QY 1 HNLGKHLNS 9

Search completed: Thu Jul 30 10:27:26 1998
 Job time : 15 secs.

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15:25
 SUMMARY

#region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 62; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.02e-03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 HNLGKHLS 14
 0Y 1 HNLGKHLS 9

Search completed: Thu Jul 30 10:26:53 1998
 Job time : 28 secs.

NWSEET (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:25:15 1998; MasPar time 2.12 Seconds
106.609 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-13
Description: (1-9) from US08817547A.pep
Percent Score: 62
Sequence: 1 HNLGKHLNS 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.158; Variance 22.443; scale 0.987

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	62	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.55e-04
2	58	93.5	115	1	PTHY_PIG PARATHYROID HORMONE PR	2.07e-03
3	58	93.5	115	1	PTHY_CANFA PARATHYROID HORMONE PR	2.07e-03
4	58	93.5	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	2.07e-03
5	57	91.9	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.90e-03
6	48	77.4	171	1	PLA_BACSU PROTEASE SYNTHASE AND	8.66e-01
7	47	75.8	621	1	JUNCTION PLAKOGLOBIN (1.52e+00
8	47	75.8	733	1	PLAK_XENLA JUNCTION PLAKOGLOBIN (1.52e+00
9	47	75.8	743	1	PLAK_HUMAN JUNCTION PLAKOGLOBIN (1.52e+00
10	45	72.6	187	1	ATPD_ODOSI ATP SYNTHASE DELTA CHA	4.57e+00
11	45	72.6	381	1	DHR2_MOUSE ESTRADIOL 17 BETA-DEHY	4.57e+00
12	44	71.0	265	1	APAL_PIG APOLIPOPROTEIN A-1 PRE	7.80e+00
13	44	71.0	317	1	KPSF_PIG KPSF PROTEIN.	7.80e+00
14	44	71.0	386	1	PROTEIN C17/B23.	7.80e+00
15	44	71.0	585	1	Y187_MYCGE FERROCHLATASE (EC 4.9	1.32e+01
16	43	69.4	310	1	HEMZ_BACSU PROBABLE NA(+)/H(+) AN	1.32e+01
17	43	69.4	985	1	YPT7_CAEEL HYPOTHETICAL 11.7 KD	1.32e+01
18	43	69.4	1021	1	YPT7_CAEEL HYPOTHETICAL 11.7 KD	1.32e+01
19	42	67.7	180	1	Y088_METUA HYPOTHETICAL PROTEIN M	2.21e+01
20	42	67.7	192	1	SC72_YEAST TRANSLOCATION PROTEIN	2.21e+01
21	42	67.7	246	1	SR1A_PHYPO SPHERULIN 1A PRECURSOR	2.21e+01
22	42	67.7	292	1	YG29_YEAST HYPOTHETICAL 34.0 KD P	2.21e+01
23	42	67.7	417	1	HS47_HUMAN 47 KD HEAT SHOCK PROTE	2.21e+01

RESULT	ID	PTHY_HUMAN	STANDARD:	PTHY	115 AA.
AC	P01270:				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	EUTHERIA; PRIMATES.				
NC	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 82150870.				
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T., RICH A.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 83169834.				
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.,				
RA	HENDY G.N., POTTS J.T., RICH A., KRONENBERG H.M.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).				
RN	[3]				
RP	SEQUENCE OF 26-37.				
RP	MEDLINE: 74174967.				
RA	JACOBS J.W., KEMPER B., NITALL H.D., HABENER J.F., POTTS J.T., JR.;				
RL	NATURE 249:155-157(1974).				
RN	[4]				
RP	SEQUENCE OF 32-68.				
RP	MEDLINE: 74111656.				
RA	NITALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,				
RA	O'RIORDAN J.L.H., AUREBACH G.D., POTTS J.T., JR.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).				
RN	[5]				
RP	SEQUENCE OF 61-83 AND 84-115.				
RP	MEDLINE: 79082855.				
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,				
RA	POTTS J.T., JR.;				
RN	BIOCHEMISTRY 17:5723-5729(1978).				
RN	[6]				
RP	SEQUENCE OF 75-100.				
RA	KEUTMANN H.T., NITALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,				
RA	O'RIORDAN J.L.H., POTTS J.T., JR.;				
RL	(IN) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.,				
RL	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,				
RL	(1975).				
RN	[7]				

RP REVISIONS.
 RX MEDLINE; 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 75059220.
 RA TEGENAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPPE-SEILER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 73327467.
 RA ANDREATTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA RINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 93345518.
 RA BARDEN J.A., CUTHERSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE; 95318084.
 RA MARY U.C., AUSTERMANN S., BAYER P., ADERMAN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE; 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 DR EMBL; J00301; G190704; -.
 DR EMBL; A28146; E186700; -.
 DR PIR; A01336; PTHU.
 DR PIR; A19339; A19339.
 PDB; 1HPH; 10-JUL-95.
 PDB; 12WA; 12-MAR-97.
 PDB; 12WB; 12-MAR-97.
 PDB; 12WC; 12-MAR-97.
 PDB; 12WD; 12-MAR-97.
 PDB; 12WE; 12-MAR-97.
 PDB; 12WF; 16-JUN-97.
 PDB; 12WG; 16-JUN-97.
 DR MIM; 146200; -.
 DR MIM; 168450; -.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KM HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA; 12861 MW; 243E87C7 CRC32;
 SO
 Query Match 100.0%; Score 62; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.55e-04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 HNLGKHLNS 48
 OY 1 HNLGKHLNS 9
 RESULT 2
 ID PTHV.PIG STANDARD; PRT; 115 AA.
 AC P01269;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 OS SUS SCROFA (PIG).
 OC EURKAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87316938.
 RA SCHMELZER H.-J., GROSS G., WIDERA G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN [2]
 RP SEQUENCE OF 26-115.
 RX MEDLINE; 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN [3]
 RP SEQUENCE OF 32-115.
 RX MEDLINE; 7423317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 RA POTTS J.T. JR.;
 RL BIOCHEMISTRY 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL; X05722; G1839; -.
 DR PIR; A01535; PTPB.
 DR PIR; B26806; B26806.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KM HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT SEQUENCE 115 AA; 12852 MW; 98B67F47 CRC32;
 SO
 Query Match 93.5%; Score 58; DB 1; Length 115;
 Best Local Similarity 88.9%; Pred. No. 2.07e-03;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: Thu Jul 30 10:25:21 1998
 Job time : 6 secs.

RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L., OVERBEEK R.,
RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T., COTTON M.D.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A.,
RA DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L.,
RA KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C., FLEISCHMANN R.D.,
RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L., OVERBEEK R.,
RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T., COTTON M.D.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
RA SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL: AB000982; G2648811; -
NM
SO SEQUENCE 421 AA; 48473 MW; D1467826 CRC32;

Query Match 79.0%; Score 49; DB 9; Length 421;
Best Local Similarity 77.8%; Pred. No. 6.15e-01;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 79 NMLSKHLNS 87
:|||||
QY 1 HNLGKHLNS 9

Search Completed: Thu Jul 30 10:26:08 1998
Job time : 30 secs.

[W][I][T][H][I][N] (TM)

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Search protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:29:27 1998; MasPar time 2.68 Seconds
45.741 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-14
Description: (1-8) from US08817547A.pep
Perfect Score: 58
Sequence: 1 HNLGKHLN 8

Scoring table:
PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.991; Variance 49.457; scale 0.303

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	58	100.0	34	9	R58241 [Nle8,18,D-Asn33,D-ph	7.41e+00
2	58	100.0	34	22	W17949 Human parathyroid hor	7.41e+00
3	58	100.0	34	22	W17958 Human parathyroid hor	7.41e+00
4	58	100.0	34	22	W17955 Human parathyroid hor	7.41e+00
5	58	100.0	34	22	W17954 Human parathyroid hor	7.41e+00
6	58	100.0	34	22	W17969 Human parathyroid hor	7.41e+00
7	58	100.0	34	22	W17970 Human parathyroid hor	7.41e+00
8	58	100.0	34	2	R07822 Human parathyroid hor	7.41e+00
9	58	100.0	34	4	P30022 Human parathyroid (1-	7.41e+00
10	58	100.0	34	22	W17943 Human parathyroid hor	7.41e+00
11	58	100.0	34	22	W19997 Cyclised [Nle 8,18, T	7.41e+00
12	58	100.0	34	22	W17948 Human parathyroid hor	7.41e+00
13	58	100.0	35	14	R74502 Parathyroid hormone p	7.41e+00
14	58	100.0	35	14	R74514 Parathyroid hormone p	7.41e+00
15	58	100.0	35	14	R74506 Parathyroid hormone p	7.41e+00
16	58	100.0	35	14	R74431 Parathyroid hormone p	7.41e+00
17	58	100.0	36	9	R58088 [1-amino-cyclopentane	7.41e+00
18	58	100.0	36	9	R58198 [D-Ser3]-hPTH(1-36)-N	7.41e+00

20	58	100.0	36	9	R58199 [D-Glu4]-hPTH(1-36)-N	7.41e+00
21	58	100.0	36	9	R58281 [D-Val12]-hPTH(1-36)-	7.41e+00
22	58	100.0	36	9	R58071 [Ala18, Glu18]-hPTH(1-	7.41e+00
23	58	100.0	36	9	R58213 [D-Ser17]-hPTH(1-36)-	7.41e+00
24	58	100.0	36	9	R58214 [Ala19]-hPTH(1-36)-NH	7.41e+00
25	58	100.0	36	9	R58263 [D-Ile5]-hPTH(1-36)-N	7.41e+00
26	58	100.0	36	2	R23995 Human parathyroid hor	7.41e+00
27	58	100.0	37	5	R24778 hPTH(1-37)-amide/ethy	7.41e+00
28	58	100.0	37	9	R58282 [Trp(SO2Pmc)23]-hPTH(7.41e+00
29	58	100.0	38	9	R58163 [Pro33]-hPTH(1-38)-OH	7.41e+00
30	58	100.0	38	9	R58121 [Met17]-hPTH(1-38)-OH	7.41e+00
31	58	100.0	38	9	R58122 [Ile17]-hPTH(1-38)-OH	7.41e+00
32	58	100.0	38	9	R58134 [Ile19]-hPTH(1-38)-OH	7.41e+00
33	58	100.0	38	9	R58166 [Lys33]-hPTH(1-38)-OH	7.41e+00
34	58	100.0	38	9	R58162 [Arg33]-hPTH(1-38)-OH	7.41e+00
35	58	100.0	44	26	P30015 Human parathyroid hor	7.41e+00
36	58	100.0	47	25	W21946 Fusion protein compri	7.41e+00
37	58	100.0	84	27	W25687 Human parathyroid hor	7.41e+00
38	58	100.0	84	25	W29420 Human parathyroid hor	7.41e+00
39	58	100.0	84	6	R30851 Genetic human parathy	7.41e+00
40	58	100.0	84	7	R34460 Human parathyroid hor	7.41e+00
41	58	100.0	84	4	R21250 Human parathyroid hor	7.41e+00
42	58	100.0	84	4	R21251 Human parathyroid hor	7.41e+00
43	58	100.0	84	4	R23245 Human parathyroid hor	7.41e+00
44	58	100.0	84	4	R21243 Human parathyroid hor	7.41e+00
45	58	100.0	115	13	R75693 Human prepro-PTH	7.41e+00

ALIGNMENTS

RESULT 1
ID R58241; 1
AC R58241; standard; peptide: 34 AA.

AD	20-SEP-1994 (first entry)
DE	[Nle8,18,D-Asn33,D-Phe34]-hPTH(1-34)NH2.
KW	Human parathyroid hormone; hPTH; variant; analogue;
KW	calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW	hypoparathyroidism.
OS	Synthetic.
FT	modified_site 8 Location/Qualifiers
FT	modified_site 18 /label= Nle
FT	modified_site 33 /label= Nle
FT	misc_difference 33 /note= "D-form residue."
FT	misc_difference 34 /note= "D-form residue."
FT	modified_site 34 /note= "in amide form"
PN	GB2269176-A.
PD	02-FEB-1994.
PF	12-JUL-1993; 014384.
PR	15-JUL-1993; GB-015009.
PR	18-DEC-1992; GB-026415.
PR	23-DEC-1992; GB-026859.
PR	23-DEC-1992; GB-026861.
PR	28-JAN-1993; GB-001691.
PR	28-JAN-1993; GB-001692.
PR	14-APR-1993; GB-007673.
PR	19-APR-1993; GB-008033.
PA	(SANO) SANDOZ LTD.
PA	(BAOE) SANDOZ PATENT GMBH.
PA	(SANO) SANDOZ PATENT GMBH.
PI	(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI	Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI	Combert F, Gram H, Lewis I, Ramage P, Schneider H;
PI	Waelchli R, Rainer A;
DR	WPI: 94-018352/03.
PT	New active para-thyroid hormone variants - used for treating or
PT	preventing osteoporosis etc.
PS	Example 239: Page 45; 92pp; English.
CC	This peptide is an example of a highly generic formula covering

Job time : 16 secs.

CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 34 AA;

Query Match 100.0%; Score 58; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.41e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhlh 16
| | | | | | | |
QY 1 HNLGKHLN 8

RESULT 2
ID W17949 standard; peptide; 34 AA.
AC W17949;

DT 29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha24,28,31]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.

OS Synthetic.
FH Key

Location/Qualifiers
modified_site 24

/label- OTHER
/note= "Cyclohexylalanine (Cha)"

modified_site 28
/label- OTHER

modified_site 31
/note= "Cha"

modified_site 34
/label- OTHER
/note= "Cha"

modified_site 34
/note= "In amide form"

PN W09702834-A1.
PD 30-JAN-1997.
PE 03-JUL-1996; U11292.
PR 13-JUL-1995; US-001105.
PR 06-SEP-1995; US-003305.
PR 29-MAR-1996; US-626186.
PA (BIOM-) BIOMEASURE INC.
PI Dong 2X;
DR WPI; 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which
PT stimulate bone growth and are used for treatment of osteoporosis and
PT bone fracture
Claim 7; Page -: 33pp; English.

The present sequence is a specific example of a human parathyroid
hormone (hPTH) analogue from fragment 1-34 in which at least one
of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31
is cyclohexylalanine (Cha). In this example the Trp residue at
position 24 and 28, and the Val residue at position 31 of the
wild-type have been substituted by Cha. The hPTH analogues stimulate
bone growth and so are useful in human or veterinary medicine for
treatment of osteoporosis and bone fracture, optionally in conjunction
with anti-resorptive therapy (bisphosphonates and calcitonin).
CC N.B. The present sequence does not appear in the specification. It
CC corresponds to the known hPTH 1-34 fragment with the modifications
CC as stated in the claim.
SQ Sequence 34 AA;

Query Match 100.0%; Score 58; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.41e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhlh 16
| | | | | | | |
QY 1 HNLGKHLN 8

Search completed: Thu Jul 30 10:29:43 1998

WIREIMAGE
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:28:51 1998; MasPar time 3.31 Seconds
Tabular output not generated. 88.370 Million cell updates/sec

Title: >US-08-817-547A-14
Description: (1-8) from US08817547A.pep
Perfect Score: 58
Sequence: 1 HNLGKHLN 8

Scoring table: PAM 150
GAP 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p156
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 20.760; Variance 25.957; scale 0.800

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	58	100.0	34	5	12WA	parathyroid hormone (1.85e-02
2	58	100.0	34	5	12WE	parathyroid hormone (1.85e-02
3	58	100.0	34	5	12WF	parathyroid hormone (1.85e-02
4	58	100.0	34	5	12WG	parathyroid hormone (1.85e-02
5	58	100.0	35	5	12WD	parathyroid hormone (1.85e-02
6	58	100.0	35	5	12WB	parathyroid hormone (1.85e-02
7	58	100.0	37	5	12RH	parathyroid hormone (1.85e-02
8	58	100.0	37	5	12RH	parathyroid hormone (1.85e-02
9	55	94.8	34	5	12RH	cyclic parathyroid hormone (1.85e-02
10	54	93.1	37	5	12WC	parathyroid hormone (1.54e-01
11	54	93.1	115	1	PTBO	parathyroid hormone (1.54e-01
12	54	93.1	115	1	PTBP	parathyroid hormone (1.54e-01
13	54	93.1	115	2	UC4202	parathyroid hormone (1.54e-01
14	53	91.4	105	2	151851	parathyroid hormone - 2.59e-01
15	53	91.4	112	2	A05091	parathyroid hormone - 2.59e-01
16	48	82.8	172	2	A35145	transcriptional regul 3.18e+00
17	48	82.8	172	2	E69671	transcriptional regul 3.18e+00
18	45	77.6	421	2	E69467	hypothetical protein 1.33e+01
19	44	75.9	231	2	U00704	apolipoprotein A-I - 2.12e+01
20	44	75.9	264	2	S31394	apolipoprotein A-I - 2.12e+01
21	44	75.9	264	2	A46018	apolipoprotein A-I - 2.12e+01
22	44	75.9	386	2	D42528	B23R protein - vaccin 2.12e+01
23	44	75.9	568	2	S76244	hypothetical protein 2.12e+01

24	44	75.9	585	2	G64220	ATP-binding protein m 2.12e+01
25	43	74.1	308	5	1AK1	ferrochelatase (EC 4. 3.35e+01
26	43	74.1	310	5	1FJ1	ferrochelatase (EC 4. 3.35e+01
27	43	74.1	310	2	C47045	ferrochelatase (EC 4. 3.35e+01
28	43	74.1	619	2	S54636	probable membrane pro 3.35e+01
29	43	74.1	621	2	S35092	plakoglobin - mouse (3.35e+01
30	43	74.1	738	2	S35093	plakoglobin - African 3.35e+01
31	43	74.1	744	2	A432905	plakoglobin, desmosom 3.35e+01
32	43	74.1	1021	2	S44644	F37A4.7 protein - Cae 3.35e+01
33	42	72.4	180	2	H64310	hypothetical protein 5.26e+01
34	42	72.4	243	2	B29624	spherulin 1b precursu 5.26e+01
35	42	72.4	292	2	S64361	hypothetical protein 5.26e+01
36	42	72.4	480	2	F69505	thymidylate synthase 5.26e+01
37	42	72.4	1447	2	S63669	ubiquitin--protein 11 5.26e+01
38	42	72.4	1950	2	S12332	polyketide synthase p 5.26e+01
39	42	72.4	4930	2	E69679	heat shock protein Hs 8.18e+01
40	41	70.7	417	1	S20608	heat shock protein Hs 8.18e+01
41	41	70.7	417	1	A40968	probable RNA-directed 8.18e+01
42	41	70.7	513	2	S21976	hypothetical protein 8.18e+01
43	41	70.7	592	2	D64044	cyclic peptide synthe 8.18e+01
44	41	70.7	1401	2	S77657	RNA-directed RNA poly 8.18e+01
45	41	70.7	1444	1	A43377	

ALIGNMENTS

RESULT	1	12WA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		HPTH(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WA	
REFERENCE		TN001717	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	
KEYWORDS		Determination: NMR	
FEATURE		hormone	
SUMMARY		#region helix (right hand alpha) \	
		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4118 #checksum 5629	
Query Match		100.0%; Score 58; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.85e-02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	9	HNLGKHLN 16	
Qy	1	HNLGKHLN 8	
RESULT	2	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15-25
 SUMMARY

#region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 58; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.85e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 HNLGKHLN 13
 QY 1 HNLGKHLN 8

Search completed: Thu Jul 30 10:29:09 1998
 Job time : 18 secs.

NBI

(TM)

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MSPRCH_DP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:27:45 1998; Maspar time 2.10 Seconds
Tabular output not generated. 95.669 Million cell updates/sec

Title: >US-08-817-547A-14
Description: (1-8) from US08817547A.pep
Perfect Score: 58
Sequence: 1 HNLGKHLN 8

Scoring table:
Gap 15
PAM 150

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 21.688; Variance 21.433; scale 1.012

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	58	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	8.80e-04
2	54	93.1	115	1	PTHY_PIG PARATHYROID HORMONE PR	1.17e-02
3	54	93.1	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.17e-02
4	54	93.1	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.17e-02
5	53	91.4	115	1	PTHY_RAT PARATHYROID HORMONE PR	2.20e-02
6	48	82.8	171	1	PAIA_BACSU PROTEASE SYNTHASE AND	4.64e-01
7	45	77.6	381	1	DHB2_MOUSE ESTRADIOL 17 BETA-DEHY	2.62e+00
8	44	75.9	265	1	APAI_PIG APOLIPOPROTEIN A-1 PRE	4.57e+00
9	44	75.9	386	1	VC17_VACCC PROTEIN C17/B23	4.57e+00
10	44	75.9	585	1	Y187_MYCGE HYPOTHETICAL ABC TRANS	4.57e+00
11	43	74.1	310	1	HEW2_BACSU FERROCHELATASE (EC 4.9	7.91e+00
12	43	74.1	621	1	PLAK_MOUSE JUNCTION PLAKGLOBIN (7.91e+00
13	43	74.1	738	1	PLAK_XENLA JUNCTION PLAKGLOBIN (7.91e+00
14	43	74.1	743	1	PLAK_HUMAN JUNCTION PLAKGLOBIN (7.91e+00
15	43	74.1	1021	1	YPT7_CAEEL HYPOTHETICAL 111.7 KD	7.91e+00
16	42	72.4	180	1	Y088_METUA HYPOTHETICAL PROTEIN M	1.36e+01
17	42	72.4	246	1	SRIA_PHYPO SPHERULIN 1A PRECURSOR	1.36e+01
18	42	72.4	246	1	YG29_YEAST HYPOTHETICAL 34.0 KD P	1.36e+01
19	42	72.4	887	1	MTG4_SCHPO 26S PROTEASOME REGULAT	1.36e+01
20	42	72.4	1950	1	UBRL_YEAST N-END-RECOGNIZING PROT	1.36e+01
21	41	70.7	105	1	YBXE_STRAUT PROBABLE RIBOSOMAL PRO	2.30e+01
22	41	70.7	187	1	ATPD_ODOST ATP SYNTHASE DELTA CHA	2.30e+01
23	41	70.7	245	1	PF1A_ECOCI PYRUVATE FORMATE-LYASE	2.30e+01

RESULT	ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	P01270;					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
NC	EUTHERIA; PRIMATES.					
CC	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 82150870.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.;					
RL	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RX	MEDLINE: 74174967.					
RA	JACOBS J.W., KEMPER B., NITAL H.D., HABENER J.F., POTTS J.T. JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RX	MEDLINE: 74111656.					
RA	NITAL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;					
RL	O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RX	MEDLINE: 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;					
RL	POTTS J.T. JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NITAL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;					
RL	O'RIORDAN J.L.H., POTTS J.T. JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.;					
RL	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGGAR G.W., VAN RIJSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPPE-STYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73327467.
 RA ANDREATTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA RINIKER B., RITTEL W., SIEBER P.,
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345518.
 RA BARDEN J.A., CUTHERSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MARK U.C., AUSTERMANN S., BAYER P., ADERMAN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE: 91009611.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 HYPOPARATHYROIDISM (FTH).
 CC EMBL: J00301; G190704; -.
 DR EMBL: V00597; G37144; -.
 DR EMBL: A29146; E186700; -.
 DR PIR: A01536; PTHU.
 DR PIR: A19339; PTHU.
 DR PDB: 1HPH; 10-JUL-95.
 DR PDB: 1HTH; 15-OCT-97.
 DR PDB: 1ZWA; 12-MAR-97.
 DR PDB: 1ZWB; 12-MAR-97.
 DR PDB: 1ZWC; 12-MAR-97.
 DR PDB: 1ZWD; 12-MAR-97.
 DR PDB: 1ZWE; 12-MAR-97.
 DR PDB: 1ZWF; 16-JUN-97.
 DR PDB: 1ZWG; 16-JUN-97.
 DR MIM: 146200; -.
 DR MIM: 168450; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA: 12861 MW: 24388767 CRC32;
 SQ

Query Match 100.0%; Score 58; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 8.80e-04;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 HNLGKHLN 47
 OY 1 HNLGKHLN 8
 RESULT 2
 ID PTHY PIG STANDARD; PRT: 115 AA.
 AC P01269;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS SUS SCROFA (PTG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87316938.
 RA SCHWEIZER H.-J., GROSS G., WIDERA G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN [2]
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN [3]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 74253317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 RA POTTS J.T. JR.;
 RL BIOCHEMISTRY 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL: X05722; G1839; -.
 DR PIR: A01535; PTPG.
 DR PIR: B26806; B26806.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT SEQUENCE 115 AA: 12852 MW: 98867P47 CRC32;
 SQ

Query Match 93.1%; Score 54; DB 1; Length 115;
 Best Local Similarity 87.5%; Pred. No. 1.17e-02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: Thu Jul 30 10:27:51 1998
 Job time : 6 secs.

WIDEOR (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:28:08 1998; MasPar time 3.81 Seconds
Tabular output not generated. 88,534 Million cell updates/sec

Title: >US-08-817-547A-14
Description: (1-8) from US08817547A.pep
Perfect Score: 58
Sequence: 1 HNLGKHLN 8

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: spltemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 20.802; Variance 21.214; scale 0.981

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	53	91.4	105	10	063473	PARATHYROID HORMONE (F	2.85e+02
2	48	82.8	172	9	032112	TRANSCRIPTIONAL REGULA	5.95e+01
3	45	77.6	381	10	062730	17-BETA HYDROXYSTEROID	3.37e+00
4	45	77.6	421	9	028532	HYPOTHETICAL 48.5 KD P	3.37e+00
5	45	77.6	1817	3	019931	COSMID F31D5.	3.37e+00
6	44	75.9	82	4	029248	APOLIPROTEIN A-I (FR	5.90e+00
7	44	75.9	96	11	072500	VPR PROTEIN.	5.90e+00
8	44	75.9	301	11	070212	ENVELOPE GLYCOPROTEIN	5.90e+00
9	44	75.9	568	9	P74405	HYPOTHETICAL 62.3 KD P	5.90e+00
10	43	74.1	123	2	014904	WNT-LIKE PROTEIN WNT14	1.02e+01
11	43	74.1	171	2	015093	PLAOGLOBIN (FRAGMENT)	1.02e+01
12	43	74.1	312	3	023212	COSMID T07E3.	1.02e+01
13	43	74.1	414	3	001906	COSMID F59E12.	1.02e+01
14	43	74.1	619	1	099234	CHROMOSOME XV READING	1.02e+01
15	43	74.1	745	2	015151	PLAOGLOBIN.	1.02e+01
16	43	74.1	745	10	P70565	PLAOGLOBIN.	1.02e+01
17	43	74.1	2272	2	015020	KIAA0302 (FRAGMENT).	1.76e+01
18	42	72.4	96	11	P88152	VPR PROTEIN.	1.76e+01
19	42	72.4	283	7	021973	HYPOTHETICAL 31.3 KD P	1.76e+01
20	42	72.4	314	11	Q84584	GENOME, PARTIAL SEQUEN	1.76e+01

RESULT	ID	PRELIMINARY	PRT	105 AA.	ALIGNMENTS
AC	063473				
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE (FRAGMENT).				
GN	PTH.				
OS	RATTUS NORVEGICUS (RAT).				
OC	EUHAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EDUAROTA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=THYROID, AND PARATHYROID;				
RA	SCHMELZER H.J., GROSS G., MAYER H.;				
RL	ADV. GENE TECHNOL. 21:228-229(1984).				
DR	EMBL; M54875; G601933; -				
FT	NON TER 1				
SO	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;				
Db	30 HNLGKHL 36				
Qy	1 HNLGKHL 7				
RESULT	2				
AC	032112	PRELIMINARY;	PRT;	172 AA.	
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				
DE	TRANSCRIPTIONAL REGULATOR.				
GN	PAFA.				
OS	BACILLUS SUBTILIS.				
OC	PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=168;				
RA	KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,				
RA	AZVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,				

RA BORRIS R., BOHRSTER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.R., CODANI J.J., CONNERTON I.F., COWINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFF A., EHRLICH S.D., EMERSON P.T.,
RA EHTIAN K.D., EHRINGTON J., FABER C., FERRARI E., FOULGER D., FRITZ C.,
RA FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N., GHIM S.Y.,
RA GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPI G., GUY B.J.,
RA HAGA K., HAIRECH J., HARWOOD C.R., HENAUT A., HILBERT H., HOLSAPPEL S.,
RA HOSONO S., HULLO M.F., IITAYA M., JONES L., JORTS B., KARAMATA D.,
RA KASHIHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y., KOETTER P.,
RA LARDINOIS S., LAUBER J., KUMANO M., KURITA K., LAPIDUS A.,
RA MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLAO R.P., MIZUNO M.,
RA MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGAMA K.,
RA OGIMAWA A., ODEGA B., PARK S.H., PARO V., POHL T.M., PORTETELLE D.,
RA RAPPOPORT G., PRESCOTT A.M., PRESCAN E., PUJIC P., PURNELLE B.,
RA ROCHE B., ROSE M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E.,
RA SCHROETER R., SCOPFONE F., SEXTIGUCHI J., SEKONSKA A., SERO S.J.,
RA SERROR P., SHIN B.S., SOLO B., SOROKIN A., TACCONE E., SCHLEICH S.,
RA TAKAHASHI H., TAKEMARU K., TAKEUCHI T., TAKAGI T.,
RA TERPSTRA P., TOGNONI A., TOSATO V., UCHIYAMA S., TANAKA T.,
RA VANIER F., VASSAROTTI A., VIARI A., WAMUTT R., WANDENBOL M.,
RA WEITZENEGGER T., WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K.,
RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZIMSTEIN E.,
RA YOSHIKAWA H., DANCHIN A.,
RL NATURE 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.,
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 299120; E1184294.
SO SEQUENCE 172 AA; 20015 MW; 2AA7F8CE CRC32;

Query Match 82.8%; Score 48; DB 9; Length 172;
Best Local Similarity 85.7%; Pred. No. 5.95e-01;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 105 HGLGKHL 111
QY 1 HNLGKHL 7

Search completed: Thu Jul 30 10:28:33 1998
Job time : 25 secs.

[W][O][R][D][S] (TM)

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MSrch_PP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:31:15 1998; MasPar time 2.62 Seconds
40.993 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-15
Description: (1-7) from US08817547A.pep
Perfect Score: 53
Sequence: 1 HNLGKHL 7

Scoring table:
PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31.2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.515; Variance 42.487; scale 0.342

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	53	100.0	28	4 R22064	Modified hPTH(7-34)NH	9.01e+00
2	53	100.0	34	26 R62432	Accelerator peptide b	9.01e+00
3	53	100.0	34	18 R88834	Human parathyroid hor	9.01e+00
4	53	100.0	34	20 W14310	Cyclic parathyroid ho	9.01e+00
5	53	100.0	34	9 R53673	Parathyroid hormone/p	9.01e+00
6	53	100.0	34	9 R45482	Parathyroid hormone/p	9.01e+00
7	53	100.0	34	8 R41581	[Arg16,17]hPTH (1-34)	9.01e+00
8	53	100.0	34	7 R41576	[Lys16]hPTH (1-34)NH2	9.01e+00
9	53	100.0	34	7 R34366	Human parathyroid hor	9.01e+00
10	53	100.0	34	7 R34367	Human parathyroid hor	9.01e+00
11	53	100.0	34	22 W17858	Human parathyroid hor	9.01e+00
12	53	100.0	34	22 W17966	Human PTH analogue [C	9.01e+00
13	53	100.0	34	22 W17957	Human parathyroid hor	9.01e+00
14	53	100.0	35	14 R74442	Parathyroid hormone p	9.01e+00
15	53	100.0	35	14 R74444	Parathyroid hormone p	9.01e+00
16	53	100.0	35	14 R74504	Parathyroid hormone p	9.01e+00
17	53	100.0	36	14 R74503	Parathyroid hormone p	9.01e+00
18	53	100.0	36	9 R58242	[Lys(isopropyl)13]-hp	9.01e+00
19	53	100.0	36	9 R58246	Acetyl-hPTH(1-36)-NH2	9.01e+00

RESULT	ID	Score	Query Match	Length	ID	Description	Pred. No.
20	53	100.0	36	9 R58221	[Nle8,18,27]-hPTH(1-3	9.01e+00	
21	53	100.0	38	9 R58161	[Pro3,Thr33]-hPTH(1-3	9.01e+00	
22	53	100.0	38	9 R58156	[Leu27]-hPTH(1-38)-OH	9.01e+00	
23	53	100.0	38	9 R58152	[Arg22]-hPTH(1-38)-OH	9.01e+00	
24	53	100.0	38	9 R58151	[Ser22]-hPTH(1-38)-OH	9.01e+00	
25	53	100.0	38	9 P20248	Parathyroid hormone 1	9.01e+00	
26	53	100.0	38	19 R98958	Target peptide (PTH(1	9.01e+00	
27	53	100.0	44	26 P30015	Human parathyroid hor	9.01e+00	
28	53	100.0	78	6 R30859	Leu8 hPTH (7-84) mute	9.01e+00	
29	53	100.0	84	27 W25687	Human parathyroid hor	9.01e+00	
30	53	100.0	84	27 R23293	Human parathyroid ho	9.01e+00	
31	53	100.0	84	7 R34458	Bovine parathyroid ho	9.01e+00	
32	53	100.0	84	4 R21215	Human parathyroid hor	9.01e+00	
33	53	100.0	84	4 R23402	Porcine parathyroid h	9.01e+00	
34	53	100.0	84	4 R23356	Bovine parathyroid ho	9.01e+00	
35	53	100.0	84	4 R21195	Human parathyroid hor	9.01e+00	
36	53	100.0	84	4 R23261	Bovine parathyroid ho	9.01e+00	
37	53	100.0	84	7 R34452	Bovine parathyroid ho	9.01e+00	
38	53	100.0	84	7 R34453	Human parathyroid hor	9.01e+00	
39	53	100.0	84	4 R23519	Bovine parathyroid ho	9.01e+00	
40	53	100.0	84	4 R23318	Human parathyroid ho	9.01e+00	
41	53	100.0	84	4 R21176	Human parathyroid hor	9.01e+00	
42	53	100.0	84	4 R23472	Porcine parathyroid h	9.01e+00	
43	53	100.0	84	4 R21212	Human parathyroid hor	9.01e+00	
44	53	100.0	84	4 R23452	Porcine parathyroid h	9.01e+00	
45	53	100.0	115	4 P40209	Sequence of prepropar	9.01e+00	

ALIGNMENTS

RESULT 1
ID R22064 standard; Protein; 28 AA.
AC R22064;
DT 14-JUL-1992 (first entry)
DE Modified hPTH(7-34)NH2.
KW Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
KM Tumours; hypercalcaemia; renal failure; human.
OS Synthetic.
FH Key
FT modified_site 7 Location/Qualifiers
FT /label= OTHER
FT /note= "OTHER - see comments"
FT modified_site 28 /label= NH2
FT FT
PN US5093233-A.
PD 03-MAR-1992.
PF 25-APR-1990; 514394.
PR 25-APR-1990; US-514394.
PA (MERT) MERCK & CO INC.
PI Rosenblatt M, Roudini E, Chouev M, Nutt RF;
DR WPI; 92-096233/12.
PT WPI parathyroid hormone analogues - useful for treatment and in
vitro diagnosis of PTH-dependent tumours, immune disorders,
PI osteoporosis and hyperparathyroidism.
PS Claim 1; Column 10; 6pp; English.
CC The peptide is modified at Lys13 (of the parent PTH) in the epsilon
amino acid gp. by N,N-disubutyl or 3-phenylpropionyl. The PTH
analogue binds with high affinity to the peptide hormone receptor
CC without activating the 2nd messenger mol. The modification of the
Lys residue stabilises the bioactive conformation of PTH to enhance
CC the activity. The peptide may be used in in vitro bioassays to
CC measure naturally occurring PTH and to diagnose the etiology of or
CC to treat osteoporosis or hypercalcaemia. It may also be used to
CC treat hyperthyroidism and diseases caused by aberrant prodn. of
CC hormone-like substances, such as tumours. It may also be used to
CC treat immune diseases such as inflammation. It is prepd. by solid
CC phase synthesis.
CC See also R22058-75.
SQ Sequence 28 AA;
Query Match 100.0%; Score 53; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.01e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 hnlgkhl 9
 |||||
 QY 1 HNLGKHL 7

RESULT

ID R62432 standard; peptide: 34 AA.
 AC R62432;
 DT 31-JUL-1995 (first entry)
 DE Accelerator peptide basic region peptide, P-8
 KW Accelerator; basic amino acid; cell growth factor; gingiva;
 KM periodontal tissue; regeneration; periodontitis; periodontal pocket;
 OS down growth; epithelium; fibre adhesion; cement.
 PN J06234653-A.
 PD 23-AUG-1994.
 PF 10-FEB-1993; JP-045998.
 PR (SUNZ) SUNSTAR CHEM IND CO LTD.
 WP1: 95-157631/21.
 Accelerator for regenerating periodontal tissue - comprises
 peptide having 3-34 aminoacid residues having connected basic
 aminoacid residues
 PT aminoacid residues
 PS Disclosure: Page 3: 7pp; Japanese.
 CC The sequences in R62425-36 are peptide fragments of an accelerator
 protein which contain at least two basic amino acids. The accelerator
 also comprises a cell growth factor. The accelerator may be used to
 accelerate the growth of periodontal tissue regeneration. The
 accelerator is applied by opening the gingiva, treating the tissue
 destroyed by periodontitis and applying the accelerator in the
 periodontal pocket. The accelerator reduces the down growth of the
 epithelium and accelerates fibre adhesion and regenerates cement.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 53; DB 26; Length 34;
 Best Local Similarity 100.0%; Pred. No. 9.01e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 9 hnlgkhl 15
 |||||
 QY 1 HNLGKHL 7

Search completed: Thu Jul 30 10:31:31 1998
 Job time : 16 secs.

WIRE (TM)

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Masrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:30:52 1998; Maspar time 4.09 Seconds
Tabular output not generated. 62.524 Million cell updates/sec

Title: >US-08-817-547A-15
Description: (1-7) from US08817547A.pep
Perfect Score: 53
Sequence: 1 HNLGKHL 7

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 20.217; Variance 24.497; scale 0.825

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	53	100.0	34	5 12WG	parathyroid hormone 4	1.17e-01
2	53	100.0	34	5 12WF	parathyroid hormone 4	1.17e-01
3	53	100.0	34	5 12WE	parathyroid hormone (1.17e-01
4	53	100.0	34	5 12WA	parathyroid hormone (1.17e-01
5	53	100.0	35	5 12WD	parathyroid hormone (1.17e-01
6	53	100.0	36	5 12WB	parathyroid hormone (1.17e-01
7	53	100.0	37	5 12WH	parathyroid hormone (1.17e-01
8	53	100.0	37	5 12WC	parathyroid hormone (1.17e-01
9	53	100.0	105	2 151851	parathyroid hormone -	1.17e-01
10	53	100.0	115	2 J04202	parathyroid hormone -	1.17e-01
11	53	100.0	115	2 A05091	parathyroid hormone P	1.17e-01
12	53	100.0	115	1 PTHU	parathyroid hormone P	1.17e-01
13	53	100.0	115	1 PTHO	parathyroid hormone P	1.17e-01
14	53	100.0	115	1 PTHG	parathyroid hormone P	1.17e-01
15	53	100.0	115	1 PTHI	parathyroid hormone P	1.17e-01
16	53	100.0	115	1 PTHJ	parathyroid hormone P	1.17e-01
17	53	100.0	115	1 PTHK	parathyroid hormone P	1.17e-01
18	53	100.0	115	1 PTHL	parathyroid hormone P	1.17e-01
19	53	100.0	115	1 PTHM	parathyroid hormone P	1.17e-01
20	53	100.0	115	1 PTHN	parathyroid hormone P	1.17e-01
21	53	100.0	115	1 PTHO	parathyroid hormone P	1.17e-01
22	53	100.0	115	1 PTHI	parathyroid hormone P	1.17e-01
23	53	100.0	115	1 PTHJ	parathyroid hormone P	1.17e-01

24	42	79.2	480	2	E69505	thymidylate synthase	3.07e+01
25	42	79.2	619	2	S54636	probable membrane pro	3.07e+01
26	41	77.4	246	2	S01789	pyruvate formate-lyase	4.89e+01
27	41	77.4	386	2	D42528	B23R protein - vaccin	4.89e+01
28	41	77.4	405	1	A41252	heat shock protein 47	4.89e+01
29	41	77.4	417	1	A42843	heat shock protein 47	4.89e+01
30	41	77.4	417	1	A40968	heat shock protein 47	4.89e+01
31	41	77.4	417	1	S20608	heat shock protein 47	4.89e+01
32	41	77.4	418	1	I52968	collig-2 - human	4.89e+01
33	41	77.4	418	1	S20608	collig-2 - human	4.89e+01
34	41	77.4	418	1	S20608	collig-2 - human	4.89e+01
35	40	75.5	160	2	E69679	polyketide synthase P	4.89e+01
36	40	75.5	180	2	H84310	probable olfactory re	7.71e+01
37	40	75.5	209	2	D51119	hypothetical protein	7.71e+01
38	40	75.5	291	2	S73826	proteasome 3,4-d	7.71e+01
39	40	75.5	292	2	E64226	MG240 homolog F10-corf	7.71e+01
40	40	75.5	421	2	E69467	hypothetical protein	7.71e+01
41	40	75.5	513	2	S21976	hypothetical protein	7.71e+01
42	40	75.5	773	2	A46627	probable RNA-directed	7.71e+01
43	40	75.5	1401	2	S77657	cyclic peptide synthet	7.71e+01
44	40	75.5	1444	1	A43377	RNA-directed RNA poly	7.71e+01
45	40	75.5	1447	2	S63669	UDPglucose--glycoprot	7.71e+01

ALIGNMENTS

RESULT	ENTRY	1	12WG	#type complete
TITLE	12WG	parathyroid hormone 4	37 mutant N-TERMINAL SUCCINYLATED -	
ALTERNATE_NAMES	synthetic	n-succinyl-hpht(4-37)		
PDB_TITLE	synthetic	synthetic		
ORGANISM	synthetic	synthetic		
REFERENCE	A67743	Roersch, P.; Marx, U.C.		
#authors	Roersch, P.; Marx, U.C.			
#submission	submitted to the Brookhaven Protein Data Bank, June 1996			
#cross-references	PDB:12WG			
REFERENCE	TN003319			
#book	Marx, U.C.			
COMMENT	Resolution: not applicable			
COMMENT	Determination: NMR			
FEATURES	KEYWORDS	disease mutation; hormone; signal		
FEATURES	2-9	#region helix (right hand alpha)		
FEATURES	15-25	#region helix (right hand alpha)		
SUMMARY	length 34	#molecular-weight 4128	#checksum 5508	
Query Match	100.0%; Score 53; DB 5; Length 34;			
Best Local Similarity	100.0%; Pred. No. 1.17e-01;			
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	6 HNLGKHL 12			
Qy	1 HNLGKHL 7			
RESULT	2	12WF	#type complete	
ENTRY	12WF	parathyroid hormone 4	37 mutant N-TERMINAL ACETYLATED -	
TITLE	synthetic	synthetic		
ALTERNATE_NAMES	n-acetyl-hpht(4-37)			
PDB_TITLE	structure of n-terminal acetylated human parathyroid hormone,			
ORGANISM	NMR, 10 structures			
REFERENCE	A67742			
#authors	Roersch, P.; Marx, U.C.			
#submission	submitted to the Brookhaven Protein Data Bank, June 1996			
#cross-references	PDB:12WF			
REFERENCE	TN003318			
#book	Marx, U.C.			
	in Strukturen Verschiedener Parathormonfragmente in Loesung,			

Thu Jul 30 13:37:57 1998

US-08-817-547A-15.rpt

Page 2

pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 53; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. NO. 1.17e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 6 HNLGKHL 12
QY 1 HNLGKHL 7

Search completed: Thu Jul 30 10:30:57 1998
Job time : 5 secs.

Search completed: Thu Jul 30 10:30:06 1998
 Job time : 5 secs.

RA BREWER H.B. JR., ROMAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 71091588.
 RA POTTS J.T. JR., TREGGAR G.W., KUTTMANN H.T., NITALL H.D., SAUER R.,
 RA DEFLOS L.J., DAMSON B.F., HOGAN M.L., AUBRACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL: V00106; G85; -.
 DR EMBL: J00023; G163641; -.
 DR EMBL: J00024; G163643; -.
 DR EMBL: J00024; E18249; ALT_SEQ.
 DR EMBL: J00024; E18250; ALT_INIT.
 DR EMBL: K01938; G163647; -.
 DR EMBL: M25082; G163645; -.
 DR PIR: A01334; PTBO.
 DR PIR: A24949; A24949.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPER 26 31
 FT CHAIN 32 115 PARATHYROID HORMONE.
 FT CONFLICT 106 106 V -> G (IN REF. 4).
 SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

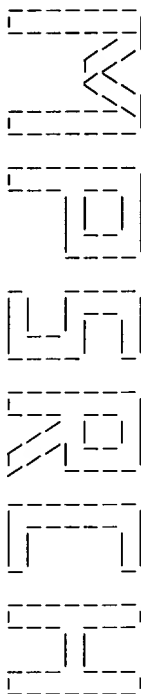
Query Match 100.0%; Score 53; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 8.04e-03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKHL 46
 QY 1 HNLGKHL 7

RESULT 2
 ID PTHY_CANFA STANDARD; PRT; 115 AA.
 AC P52212;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS CANIS FAMILIARIS (DOG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUHERETIA; CARNIVORA.
 RN [1]
 RN SEQUENCE FROM N.A.
 RN TISSUE-PARATHYROID.
 RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
 RA DEWITTE J.W., CAPEN C.C.;
 RL GENE 160:241-243(1995).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL: U15662; G558916; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR HORMONE; SIGNAL.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPER 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;

Query Match 100.0%; Score 53; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 8.04e-03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKHL 46
 QY 1 HNLGKHL 7



(TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:30:24 1998; MasPar time 3.61 Seconds
Tabular output not generated. 81.661 Million cell updates/sec

Title: >US-08-817-547A-15
Description: (1-7) from US08817547A.pep
Perfect Score: 53
Sequence: 1 HNLGKHL 7

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 20.260; Variance 20.374; scale 0.994

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	53	100.0	105 10	063473	PARATHYROID HORMONE (F	1.38e-02
2	48	90.6	172 9	032112	TRANSCRIPTIOMAL REGULA	3.17e-01
3	44	83.0	96 11	072500	VPR PROTEIN.	3.38e+00
4	43	81.1	171 2	015093	PLAOGLOBIN (FRAGMENT)	5.98e+00
5	43	81.1	312 3	022312	COSMID T07E3.	5.98e+00
6	43	81.1	745 2	015151	PLAOGLOBIN.	5.98e+00
7	43	81.1	745 10	P70565	PLAOGLOBIN.	5.98e+00
8	43	81.1	2272 2	015020	KIAA0302 (FRAGMENT).	5.98e+00
9	42	79.2	96 11	P88152	VPR PROTEIN.	1.05e+01
10	42	79.2	123 2	014904	WNT-LIKE PROTEIN WNT14	1.05e+01
11	42	79.2	381 10	062730	17-BETA HYDROXYSTEROID	1.05e+01
12	42	79.2	480 9	028232	THYMIDYLATE SYNTHASE.	1.05e+01
13	42	79.2	619 1	098234	CHROMOSOME XV READING	1.05e+01
14	42	79.2	979 8	P93820	HYPOTHETICAL 110.0 KD	1.05e+01
15	42	79.2	283 7	021973	HYPOTHETICAL 31.3 KD P	1.82e+01
16	41	77.4	404 12	090420	47 KDA HEAT SHOCK PROT	1.82e+01
17	41	77.4	568 9	P74405	HYPOTHETICAL 62.3 KD P	1.82e+01
18	41	77.4	4930 9	031783	POLYKETIDE SYNTHASE OF	1.82e+01
19	40	75.5	41 4	029179	CARANTHINE PALMITOYLTR	3.12e+01
20	40	75.5	95 11	037116	ENVELOPE GLYCOPROTEIN	3.12e+01

21	40	75.5	96 11	079793	ISOLATE NR5, COMPLETE	3.12e+01
22	40	75.5	96 11	079233	VPR PROTEIN.	3.12e+01
23	40	75.5	96 11	079249	VPR PROTEIN.	3.12e+01
24	40	75.5	160 10	062336	OLFACTORY RECEPTOR 33	3.12e+01
25	40	75.5	367 10	063778	HYPOTHETICAL 43.7 KD P	3.12e+01
26	40	75.5	421 9	028532	HYPOTHETICAL 48.5 KD P	3.12e+01
27	40	75.5	440 9	P77814	PROLIDASE (EC 3.4.13.9	3.12e+01
28	40	75.5	513 10	063289	L1 RETROPOSON, ORF2 MR	3.12e+01
29	40	75.5	563 9	048722	RELAXASE.	3.12e+01
30	40	75.5	576 2	041447	KIAA0134 PROTEIN (KIAA	3.12e+01
31	40	75.5	584 9	048665	MOBILISATION PROTEIN.	3.12e+01
32	40	75.5	643 10	035948	HOMOLOG OF HUMAN WEENE	3.12e+01
33	40	75.5	764 10	035288	CARITINE PALMITOYLTRA	3.12e+01
34	40	75.5	831 1	013705	HYPOTHETICAL 95.0 KD P	3.12e+01
35	40	75.5	833 1	013620	HYPOTHETICAL 93.7 KD P	3.12e+01
36	40	75.5	1300 10	P97692	L1 RETROTRANSPOSON ORF	3.12e+01
37	40	75.5	1401 10	009053	WERNER SYNDROME.	3.12e+01
38	40	75.5	1401 9	050177	PROBABLE CYCLIC SYNTH	3.12e+01
39	40	75.5	1444 11	038631	RNA-DEPENDENT RNA POLY	3.12e+01
40	40	75.5	1447 1	009140	UDP-GLC:GLYCOPROTEIN G	3.12e+01
41	40	75.5	1817 3	019931	COSMID F31D5.	3.12e+01
42	39	73.6	191 10	061633	EN-2/LACZ FUSION PROTE	5.31e+01
43	39	73.6	453 11	083077	BETA-B PROTEIN.	5.31e+01
44	39	73.6	480 12	090220	PREPRO-HAIXSTRATIN PREC	5.31e+01
45	39	73.6	534 9	060171	MODIFICATION METHYLASE	5.31e+01

ALIGNMENTS

RESULT	ID	Query Match	Best Local Similarity	Score	DB	Length
1	063473	100.0%	100.0%	53	10	105
PRELIMINARY:	PRT:	105 AA.				
AC	063473					
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)					
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE (FRAGMENT).					
GN	PTH.					
OS	RATUUS NORVEGICUS (RAT).					
OC	EUROTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; RODENTIA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-THYROID, AND PARATHYROID;					
RA	SCHMELZER H.J., GROSS G., MAYER H.;					
RL	ADV. GENE TECHNOL. 21:228-229(1984).					
DR	EMBL; M54875; G601933; -.					
FT	NON TER 1					
SQ	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;					
Query Match		100.0%	Score 53;	DB 10;	Length 105;	
Best Local Similarity		100.0%	Pred. No. 1.38e-02;			
Matches	7;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Db	30 HNLGKHL 36					
QY	1 HNLGKHL 7					
RESULT	2					
ID	032112	PRELIMINARY:	PRT:	172 AA.		
AC	032112					
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	TRANSCRIPTIOMAL REGULATOR.					
GN	PATA.					
OS	BACILLUS SUBTILIS.					
OC	PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-168;					
RA	KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,					
RA	AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,					

[W][I][T][H][I][N] (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:33:38 1998; Maspar time 2.52 Seconds
36.475 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-16
Description: (1-6) from US08817547A.pep
Perfect Score: 45
Sequence: 1 HNLGRK 6

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.446; Variance 33.754; scale 0.398

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description	Pred. No.
1	45	100.0	9 18	R91656	Human parathyroid hor	1.82e+01
2	45	100.0	32 18	R88840	Human parathyroid hor	1.82e+01
3	45	100.0	34 26	R62432	Accelerator peptide b	1.82e+01
4	45	100.0	34 7	R34337	Bovine parathyroid hor	1.82e+01
5	45	100.0	34 7	R34339	Bovine parathyroid hor	1.82e+01
6	45	100.0	34 18	R88834	Human parathyroid hor	1.82e+01
7	45	100.0	34 3	P82177	Sequence of parathyro	1.82e+01
8	45	100.0	34 2	R07918	Bovine parathyroid ho	1.82e+01
9	45	100.0	34 4	R22291	Human parathyroid hor	1.82e+01
10	45	100.0	34 4	R22293	Human parathyroid hor	1.82e+01
11	45	100.0	34 14	R74521	Human parathyroid hor	1.82e+01
12	45	100.0	34 7	R34366	Human parathyroid hor	1.82e+01
13	45	100.0	34 9	R58034	Isopropyl-118, K1scor	1.82e+01
14	45	100.0	34 22	W17958	Human parathyroid hor	1.82e+01
15	45	100.0	34 22	W17953	Human parathyroid hor	1.82e+01
16	45	100.0	34 22	W17957	Human parathyroid hor	1.82e+01
17	45	100.0	35 14	R74527	Human parathyroid hor	1.82e+01
18	45	100.0	36 9	R58242	[Lys(isopropyl)13]-NP	1.82e+01
19	45	100.0	36 9	R58246	Acetyl-hPTH(1-36)-NH2	1.82e+01

20	45	100.0	36 9	R58257	[Proparglylglycyl]-hP	1.82e+01
21	45	100.0	36 9	R58238	[D-Asp30]-hPTH(1-36)-	1.82e+01
22	45	100.0	38 9	P20248	Parathyroid hormone 1-3	1.82e+01
23	45	100.0	38 9	R58283	[Trp(Pmc)23]-hPTH(1-3	1.82e+01
24	45	100.0	38 9	R58036	[Gln16]-hPTH(1-38)-OH	1.82e+01
25	45	100.0	44 26	P30015	Human parathyroid hor	1.82e+01
26	45	100.0	84 27	W25687	Human parathyroid hor	1.82e+01
27	45	100.0	84 4	R23357	Bovine parathyroid ho	1.82e+01
28	45	100.0	84 4	R23266	Bovine parathyroid ho	1.82e+01
29	45	100.0	84 4	R23449	Porcine parathyroid ho	1.82e+01
30	45	100.0	84 4	R23287	Bovine parathyroid ho	1.82e+01
31	45	100.0	84 5	R29554	Oxidation resistant [1.82e+01
32	45	100.0	84 5	R29567	Oxidation resistant [1.82e+01
33	45	100.0	84 4	R21154	Human parathyroid hor	1.82e+01
34	45	100.0	84 4	R23291	Porcine parathyroid h	1.82e+01
35	45	100.0	84 4	R23285	Bovine parathyroid ho	1.82e+01
36	45	100.0	84 4	R23393	Porcine parathyroid h	1.82e+01
37	45	100.0	84 4	R23274	Bovine parathyroid ho	1.82e+01
38	45	100.0	84 4	R23284	Bovine parathyroid ho	1.82e+01
39	45	100.0	84 4	R23513	Bovine parathyroid ho	1.82e+01
40	45	100.0	84 4	R23285	Bovine parathyroid ho	1.82e+01
41	45	100.0	84 4	R23413	Porcine parathyroid h	1.82e+01
42	45	100.0	84 4	R23280	Bovine parathyroid ho	1.82e+01
43	45	100.0	84 4	R23468	Porcine parathyroid h	1.82e+01
44	45	100.0	84 4	R21212	Human parathyroid hor	1.82e+01
45	45	100.0	115 1	P80305	Sequence of human par	1.82e+01

ALIGNMENTS

RESULT 1
ID R91656 Standard; peptide: 9 AA.
AC R91656;
DT 06-NOV-1996 (first entry)
DE Human parathyroid hormone antigenic peptide hPTH 9-17.
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KM diagnosis: active hPTH 1-37.
OS Synthetic.
PN DE4434551-AA.
PD 04-APR-1996.
PF 28-SEP-1994; 434551.
PR 28-SEP-1994; DE-434551.
PA (FORS.) FORSMANN W.
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
DR WPI; 96-180391/19.
PT New antigenic peptide(s) from human parathyroid hormone - and
PT antibodies generated using them, able to distinguish between active
PT and inactive forms of the hormone
PS Claim 2; Page 5; Spp; German.
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or
CC C-terminal alpha-helical region and/or the non-structured region of
CC the hormone. Antibodies and their binding fragments generated by
CC injecting an animal with the peptides are useful as diagnostic
CC reagents for determination of biologically active hPTH(1-37).
SQ Sequence 9 AA.
Query Match 100.0%; Score 45; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.82e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 hnlgrk 6
Qy 1 HNLGRK 6
RESULT 2
ID R88840 Standard; peptide: 32 AA.
AC R88840;
DT 07-OCT-1996 (first entry)
DE Human parathyroid hormone analogue, [Leu27]-hPTH(1-32)-NH2.
KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;
KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenyl cyclase activity; cAMPase; bone loss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_site 32
 PN CA2126299-A. /note- "amidated"
 PD 21-DEC-1995.
 PE 20-JUN-1994; 126299.
 PR 20-JUN-1994; CA-126299.
 PA (WILL/) WILLICK G E.
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 DR WPI; 96-151754/16.
 PT New human parathyroid hormone analogues - which have increased
 PT adenyl cyclase activating activity, used for treating osteoporosis
 PS Claim 2; Page -, 21pp; English.
 CC R88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 SQ Sequence 32 AA;

Query Match 100.0%; Score 45; DB 18; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.82e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 9 hnlgrh 14
 |||||
 Oy 1 HNLGRH 6

Search completed: Thu Jul 30 10:33:53 1998
 Job time : 15 secs.

W I S E N E I F
***** (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:33:02 1998; MasPar time 3.01 Seconds
Tabular output not generated. 72.782 Million cell updates/sec

Title: >US-08-817-547A-16
Description: (1-6) from US08817547A.pap
Perfect Score: 45
Sequence: 1 HNLGKH 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 18.479; Variance 19.656; scale 0.940

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	45	100.0	34	5	12WG parathyroid hormone 4	5.80e-01
2	45	100.0	34	5	12WF parathyroid hormone 4	5.80e-01
3	45	100.0	34	5	12WE parathyroid hormone (5.80e-01
4	45	100.0	34	5	12WA parathyroid hormone (5.80e-01
5	45	100.0	35	5	12WD parathyroid hormone (5.80e-01
6	45	100.0	36	5	12WB parathyroid hormone (5.80e-01
7	45	100.0	37	5	12WH parathyroid hormone (5.80e-01
8	45	100.0	37	5	12WC parathyroid hormone (5.80e-01
9	45	100.0	105	2	151851 parathyroid hormone -	5.80e-01
10	45	100.0	115	2	JC4202 parathyroid hormone -	5.80e-01
11	45	100.0	115	2	A05091 parathyroid hormone p	5.80e-01
12	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
13	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
14	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
15	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
16	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
17	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
18	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
19	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
20	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
21	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
22	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01
23	45	100.0	115	1	PTHU parathyroid hormone p	5.80e-01

24	37	82.2	116	2	A58566 nerve growth factor -	4.93e+01
25	37	82.2	116	1	NGNXXI nerve growth factor -	4.93e+01
26	37	82.2	116	2	S13965 nerve growth factor -	4.93e+01
27	37	82.2	119	2	A34937 parathyroid hormone p	4.93e+01
28	37	82.2	232	2	I46679 alpha-smooth muscle a	4.93e+01
29	37	82.2	330	1	WNECH photocytotoxic reacti	4.93e+01
30	37	82.2	534	2	S61228 DNA (cytosine-5'-)met	4.93e+01
31	37	82.2	633	2	JQ1242 viral replicase 2 - b	4.93e+01
32	37	82.2	1097	2	A29943 Toll protein precuro	4.93e+01
33	37	82.2	1938	1	MMK1 myosin heavy chain D	4.93e+01
34	37	82.2	1947	1	S05697 myosin heavy chain C	4.93e+01
35	37	82.2	1966	1	MMK1 myosin heavy chain B	4.93e+01
36	37	82.2	1969	1	S02771 myosin heavy chain A	4.93e+01
37	36	80.0	60	2	E69209 conserved hypothetical	8.24e+01
38	36	80.0	123	2	S75382 conserved hypothetical	8.24e+01
39	36	80.0	130	2	B37059 creatine kinase (EC 2	8.24e+01
40	36	80.0	403	2	B69196 conserved hypothetical	8.24e+01
41	36	80.0	540	1	ORHUCR sn-glycerol-3-phospha	8.24e+01
42	36	80.0	586	2	S73346 No-on-transient A pro	8.24e+01
43	36	80.0	700	2	JH0162 methylenetetrahydrofo	8.24e+01
44	36	80.0	933	2	S53523 chromosome disjunctio	8.24e+01
45	36	80.0	1209	2	A49440	

ALIGNMENTS

RESULT 1	12WG	#type complete
ENTRY	parathyroid hormone 4	37 mutant N-TERMINAL SUCCINYLATED -
TITLE	synthetic	
ALTERNATE_NAMES	n-succinyl-hPTH(4-37)	
PDB_TITLE	succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM	#formal_name synthetic	
REFERENCE	A67743	
#authors	Roesch, P.; Marx, U.C.	
#submission	Submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references	PDB:12WG	
REFERENCE	TN003319	
#authors	Marx, U.C.	
#book	In Strukturen Verschiedener Parathormonfragmente in Loessung, pp. 0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT	Resolution: not applicable	
COMMENT	Determination: NMR	
KEYWORDS	disease mutation; hormone; signal	
FEATURE		
2-9	#region helix (right hand alpha)\	
15-25	#region helix (right hand alpha)	
SUMMARY	#length 34 #molecular-weight 4128 #checksum 5508	
Query Match	100.0%; Score 45; DB 5; Length 34;	
Best Local Similarity	100.0%; Pred. No. 5.80e-01;	
Matches	6; Conservative 0; Mismatches 0; Gaps 0;	
Db	6 HNLGKH 11	
Qy	1 HNLGKH 6	
RESULT 2	12WF	#type complete
ENTRY	parathyroid hormone 4	37 mutant N-TERMINAL ACETYLATED -
TITLE	synthetic	
ALTERNATE_NAMES	n-acetyl-hPTH(4-37)	
PDB_TITLE	structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures	
ORGANISM	#formal_name synthetic	
REFERENCE	A67742	
#authors	Roesch, P.; Marx, U.C.	
#submission	Submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references	PDB:12WF	
REFERENCE	TN003318	
#authors	Marx, U.C.	
#book	In Strukturen Verschiedener Parathormonfragmente in Loessung,	

Thu Jul 30 13:37:58 1998

US-08-817-547A-16.rpt

COMMENT Resolution: not applicable
pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
KEYWORDS Determination: NMR
FEATURE disease mutation: hormone; signal
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
SUMMARY #length 34 #molecular weight 4128 #checksum 5508
Query Match 100.0%; Score 45; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.80e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 6 HNLGRH 11
0y 1 HNLGRH 6

Search completed: Thu Jul 30 10:33:20 1998
Time : 18 secs.

MUSE

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:31:49 1998; MasPar time 2.04 Seconds
Tabular output not generated. 73.883 Million cell updates/sec

Title: >US-08-817-547A-16
Description: (1-6) from US08817547A.pep
Perfect Score: 45
Sequence: 1 HNLGKH 6

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 19.288; Variance 15.923; scale 1.211

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.







SUMMARIES

Built No.	Score	Query Match	Length	ID	Description	Pred. No.
1	45	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.76e-02
2	45	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.76e-02
3	45	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.76e-02
4	45	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.76e-02
5	45	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	4.76e-02
6	43	95.6	1021	1	PTHY_HUMAN PARATHYROID HORMONE PR	2.00e-01
7	41	91.1	245	1	YPT7_CAELI PYRUVATE FORMATE-LYASE	8.04e-01
8	40	88.9	105	1	YBXE_SPAU PROBABLE RIBOSOMAL PRO	1.58e+00
9	40	88.9	171	1	PATA_BACSU PROTEIN SYNTHASE AND	1.58e+00
10	39	86.7	386	1	VC17_VACCC PROTEIN C17/B23	3.08e+00
11	39	86.7	480	1	DISA_TRIGA PUTATIVE VENOM METALLO	3.08e+00
12	38	84.4	96	1	VPR_HVINS VPR PROTEIN (R ORF PRO	5.90e+00
13	38	84.4	614	1	YQ22_CAELI HYPOTHETICAL 69.0 KD P	5.90e+00
14	37	82.2	116	1	NGF_NAFAT NERVE GROWTH FACTOR (N	1.12e+01
15	37	82.2	116	1	NGF_NAFAT NERVE GROWTH FACTOR (N	1.12e+01
16	37	82.2	119	1	PTHY_CHICK PARATHYROID HORMONE PR	1.12e+01
17	37	82.2	308	1	PADI_SCHPO PADI PROTEIN	1.12e+01
18	37	82.2	330	1	RCEK_EKYSF REACTION CENTER PROTEI	1.12e+01
19	37	82.2	1097	1	TOLL_DROME TOLL PROTEIN PRECURSOR	1.12e+01
20	37	82.2	1938	1	MYSD_CAELI MYOSIN HEAVY CHAIN D	1.12e+01
21	37	82.2	1947	1	MYSD_CAELI MYOSIN HEAVY CHAIN C	1.12e+01
22	37	82.2	1966	1	MYSB_CAELI MYOSIN HEAVY CHAIN B	1.12e+01
23	37	82.2	1969	1	MYSA_CAELI MYOSIN HEAVY CHAIN A	1.12e+01

RESULT	ID	PTHY_BOVIN	STANDARD	PRT	ALIGNMENTS
AC	P01268	21-JUL-1986 (REL. 01, CREATED)		115 AA.	
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUFARYOTA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA;				
OC	EUTHERIA, ARTIODACTYLA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 80056617.				
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,				
RA	POTTS J.T. JR., RICH A.,				
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 82037785.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 83105964.				
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;				
RL	GENE 28:319-329(1984).				
RN	[5]				
RP	SEQUENCE OF 26-115.				
RP	MEDLINE: 74142666.				
RA	HAMILTON J.W., NITALL H.D., JACOBS J.W., KEUTTMANN H.T., POTTS J.T. JR.,				
RA	COHN D.V.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).				
RN	[6]				
RP	SEQUENCE OF 32-115.				
RP	MEDLINE: 71076162.				
RA	NITALL H.D., KEUTTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,				
RA	AURBACH G.D., POTTS J.T. JR.;				
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).				
RN	[7]				
RP	SEQUENCE OF 32-115.				
RP	MEDLINE: 71063634.				

Search completed: Thu Jul 30 10:31:56 1998
Job time : 7 secs.

```
RA BREWER H.B. JR., RONAN R.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).  
RN [8]  
RP SYNTHESIS OF 32-65.  
RA MEDLINE: 71091588.  
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,  
RA DEFLOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.,  
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL; J00023; G163641; -;  
DR EMBL; J00024; G163643; -;  
DR EMBL; J00024; E18249; ALT_SEQ.  
DR EMBL; J00024; E18250; ALT_SEQ.  
DR EMBL; K01938; G163647; -;  
DR EMBL; M25082; G163645; -;  
DR PIR; A01534; PTBO.  
DR PIR; A24949; A24949.  
DR PROSITE; PS00335; PARATHYROID; 1.  
DR HORMONE; SIGNAL.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 115  
FT CONFLICT 106 106  
SQ SEQUENCE 115 AA; 12980 MW; 673E45F2 CRC32;  
V -> G (IN REF. 4).  
PARATHYROID HORMONE.  
Query Match 100.0%; Score 45; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4,76e-02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 40 HNLGKH 45  
OY 1 HNLGKH 6  
RESULT 2  
ID PTH_CANFA STANDARD; PRT: 115 AA.  
AC P52212;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).  
GN PTH.  
OS CANIS FAMILIARIS (DOG).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; CARNIVORA.  
RA [1]  
RA SEQUENCE FROM N.A.  
RA TISSUE-PARATHYROID;  
RA MEDLINE; 95369696.  
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,  
RA DEWILLE J.W., CAPEN C.C.;  
RL GENE 160:241-243(1995).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL; U15662; G558916; -;  
DR PROSITE; PS00335; PARATHYROID; 1.  
DR HORMONE; SIGNAL.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 115  
FT CONFLICT 106 106  
SQ SEQUENCE 115 AA; 12957 MW; 16ED0BEC CRC32;  
BY SIMILARITY.  
BY SIMILARITY.  
PARATHYROID HORMONE.  
Query Match 100.0%; Score 45; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4,76e-02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 40 HNLGKH 45  
OY 1 HNLGKH 6
```

(TM)

RA SALMINEN M.O., KOCH C., SANDERS-BUELL E., EHRENBURG P.K.,
 RA MICHAEL N.L., CARR J.K., BURKE D.S., MCCUTCHAN F.E.,
 RL VIROLOGY 213:80-86(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NL4-3;
 RX MEDLINE; 86281827.
 RA ADACHI A., GENDELMAN H.E., KOENIG S., FOLKS T., WILLEY R.,
 RA RABSON A., MARTIN M.A.,
 RL J. VIROL. 59:284-291(1986).
 DR EMBL; D26942; G902802; -.
 FT CONFLICT 44 44 R -> Q (IN REF. 2)
 SQ SEQUENCE 96 AA; 11391 MW; 035C4D75 CRC32;
 Query Match 93.3%; Score 42; DB 11; Length 96;
 Best Local Similarity 83.3%; Pied.No. 8.18e-01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 40 HNLGRH 45
 1 HNLGRH 6

Search completed: Thu Jul 30 10:32:45 1998
 Job time : 33 secs.

MUSE

(TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:36:04 1998; MasPar time 2.57 Seconds
29.790 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-17
Description: (1-5) from US08817547A.pep
Perfect Score: 36
Sequence: 1 HNLGK 5

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.815; Variance 28.014; scale 0.457
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description	Pred. No.
1	36	100.0	34 26	R62432	Accelerator peptide b	1.04e+02
2	36	100.0	34 9	R58189	[F23,H25,H26,L27,I28, Lys15,I16 H1s27]hPTH	1.04e+02
3	36	100.0	34 8	R41568	[Lys15,I16 H1s27]hPTH	1.04e+02
4	36	100.0	34 9	R58187	[Phe23,H1s25,H1s26,Le	1.04e+02
5	36	100.0	34 7	R34455	Bovine parathyroid ho	1.04e+02
6	36	100.0	34 7	R34457	Human parathyroid ho	1.04e+02
7	36	100.0	34 22	W17958	Human parathyroid hor	1.04e+02
8	36	100.0	34 22	W17953	Human parathyroid hor	1.04e+02
9	36	100.0	34 22	W17957	Human parathyroid hor	1.04e+02
10	36	100.0	35 14	R74490	Parathyroid hormone p	1.04e+02
11	36	100.0	35 14	R74489	Parathyroid hormone p	1.04e+02
12	36	100.0	36 9	R58060	[L8,A16,Q18,A19,R22] [L8,Q18]-hPTH(1-36)-O	1.04e+02
13	36	100.0	36 9	R58055	[L8,Q18]-hPTH(1-36)-O	1.04e+02
14	36	100.0	36 9	R58186	[Pro33]-hPTH(1-38)-NH	1.04e+02
15	36	100.0	38 9	R58163	[Pro33]-hPTH(1-38)-OH	1.04e+02
16	36	100.0	38 9	R58165	[I1e33]-hPTH(1-38)-OH	1.04e+02
17	36	100.0	38 9	R58061	[I1e33]-hPTH(1-38)-OH	1.04e+02
18	36	100.0	38 9	R58147	[H1s22]-hPTH(1-38)-OH	1.04e+02
19	36	100.0	38 9	R58126	[Ala19]-hPTH(1-38)-OH	1.04e+02

20	36	100.0	38 9	R58124	[Lys19]-hPTH(1-38)-OH	1.04e+02
21	36	100.0	38 9	R58105	[Val14]-hPTH(1-38)-OH	1.04e+02
22	36	100.0	38 9	R58108	[Arg14]-hPTH(1-38)-OH	1.04e+02
23	36	100.0	38 9	R58077	[Leu33]-hPTH(1-38)-OH	1.04e+02
24	36	100.0	38 9	R58078	[Gly33]-hPTH(1-38)-OH	1.04e+02
25	36	100.0	44 26	P30015	Human parathyroid hor	1.04e+02
26	36	100.0	84 27	W25687	Human parathyroid hor	1.04e+02
27	36	100.0	84 4	R23430	Porcine parathyroid h	1.04e+02
28	36	100.0	84 4	R23263	Bovine parathyroid ho	1.04e+02
29	36	100.0	84 4	R23422	Porcine parathyroid h	1.04e+02
30	36	100.0	84 4	R23413	Porcine parathyroid h	1.04e+02
31	36	100.0	84 8	R42069	Stability-enhanced hu	1.04e+02
32	36	100.0	84 5	R29562	Oxidation resistant p	1.04e+02
33	36	100.0	84 5	R29561	Oxidation resistant p	1.04e+02
34	36	100.0	84 4	R23367	Bovine parathyroid ho	1.04e+02
35	36	100.0	84 4	R23349	Bovine parathyroid ho	1.04e+02
36	36	100.0	84 4	R23393	Porcine parathyroid h	1.04e+02
37	36	100.0	84 4	R23274	Bovine parathyroid ho	1.04e+02
38	36	100.0	84 4	R23485	Porcine parathyroid ho	1.04e+02
39	36	100.0	84 4	R23261	Bovine parathyroid ho	1.04e+02
40	36	100.0	84 4	R21162	Human parathyroid hor	1.04e+02
41	36	100.0	84 4	R21163	Human parathyroid hor	1.04e+02
42	36	100.0	84 4	R23477	Porcine parathyroid h	1.04e+02
43	36	100.0	84 4	R23476	Porcine parathyroid h	1.04e+02
44	36	100.0	84 4	R23405	Porcine parathyroid h	1.04e+02
45	36	100.0	84 4	R23297	Bovine parathyroid ho	1.04e+02

ALIGNMENTS

RESULT 1
ID R62432 standard; peptide; 34 AA.

AC R62432;
DT 31-JUL-1995 (first entry)

DE Accelerator peptide basic region peptide, P-8.
KW Accelerator; basic amino acid; cell growth factor; gingiva;
KW periodontal tissue; regeneration; periodontitis; periodontal pocket;
KW down growth; epithelium; fibre adhesion; cement.

OS Synthetic.
PN J06234653-A.
PD 23-AUG-1994.
PF 10-FEB-1993; 045998.
PR 10-FEB-1993; JP-045998.
PA (SUNZ) SUNSTAR CHEM IND CO LTD.
DR WPI: 95-157631/21.

PT Accelerator for regenerating periodontal tissue - comprises
PT peptide having 3-34 aminoacid residues having connected basic
PT aminoacid residues
PS Disclosure, Page 3; 7pp; Japanese.
CC The sequences in R62425-36 are peptide fragments of an accelerator
CC protein which contain at least two basic amino acids. The accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerate the growth of periodontal tissue regeneration. The
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC periodontal pocket. The accelerator reduces the down growth of the
CC epithelium and accelerates fibre adhesion and regenerates cement.

Sequence 34 AA:
Query Match 100.0%; Score 36; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.04e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgk 13
Qy 1 HNLGK 5

RESULT 2
ID R58189 standard; peptide; 34 AA.
AC R58189;
DT 20-SEP-1994 (first entry)
DE [F23,H25,H26,L27,I28,A29,E30,I31,T33,A34]-hPTH(1-34)-NH2.

KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteoporosis;
 OS hypoparathyroidism.
 OS Synthetic.
 FH Key
 FT modified_site 34 Location/Qualifiers
 PN GB2269176-A.
 PD 02-FEB-1994. /note= "in amide form"
 PF 12-JUL-1994.
 PR 15-JUL-1993; 014384.
 PR 18-DEC-1992; GB-015009.
 PR 23-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 (BAUE/) BAUER W.
 (SANO) SANDOZ PATENT GMBH.
 (SANO) SANDOZ-ERFINDUNGEN VERW GRS MBH.
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert P, Gram H, Lewis I, Ramage P, Schneider H;
 DR WPI: 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 preventing osteoporosis etc.
 PS Example 187; Page 44; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 34 AA;

Query Match
 Best Local Similarity 100.0%; Score 36; DB 9; Length 34;
 Matches 5; Conservative 0; Pred.NO. 1.04e+02;
 Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgk 13
 |||||
 QY 1 hnlgk 5

Search completed: Thu Jul 30 10:36:20 1998
 Job time : 16 secs.

WIDEORL (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:35:29 1998; MasPar time 2.99 Seconds
61.109 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-17
Description: (1-5) from US08817547A.pep
Perfect Score: 36
Sequence: 1 HNLGK 5

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plf56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 17.484; Variance 16.519; scale 1.058

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	36	100.0	34	5	12WG	1.89e+01
2	36	100.0	34	5	12WF	1.89e+01
3	36	100.0	34	5	12WE	1.89e+01
4	36	100.0	34	5	12WA	1.89e+01
5	36	100.0	35	5	12WD	1.89e+01
6	36	100.0	35	5	12WB	1.89e+01
7	36	100.0	37	5	12WP	1.89e+01
8	36	100.0	37	5	12WC	1.89e+01
9	36	100.0	105	2	151851	1.89e+01
10	36	100.0	115	1	PTPG	1.89e+01
11	36	100.0	115	2	JC4202	1.89e+01
12	36	100.0	115	2	A05091	1.89e+01
13	36	100.0	115	1	PTBO	1.89e+01
14	36	100.0	115	1	PTBU	1.89e+01
15	36	100.0	123	2	S75382	1.89e+01
16	36	100.0	894	2	B42372	1.89e+01
17	36	100.0	1097	2	J00301	1.89e+01
18	36	100.0	1172	2	S42622	1.89e+01
19	36	100.0	1209	2	A49440	1.89e+01
20	34	94.4	142	1	C70059	6.05e+01
21	34	94.4	146	1	HBH	6.05e+01
22	34	94.4	146	1	HBZ	6.05e+01
23	34	94.4	146	2	JU0163	6.05e+01

24	34	94.4	147	2	S22336	hemoglobin beta chain	6.05e+01
25	34	94.4	314	2	G69818	CMP-binding factor ho	6.05e+01
26	34	94.4	348	1	F69831	iron(III) dicitrate-b	6.05e+01
27	34	94.4	412	1	RNECTA	tRNA adenylyltransfer	6.05e+01
28	34	94.4	416	2	B64132	tRNA adenylyltransfer	6.05e+01
29	34	94.4	573	1	HHRT60	chaperonin groEL prec	6.05e+01
30	34	94.4	573	1	A32800	chaperonin groEL prec	6.05e+01
31	34	94.4	573	1	HHMS60	chaperonin groEL prec	6.05e+01
32	34	94.4	573	1	A34173	chaperonin groEL prec	6.05e+01
33	34	94.4	711	2	E69953	hypothetical protein	6.05e+01
34	34	94.4	759	2	G69258	ATP-dependent RNA hel	6.05e+01
35	34	94.4	830	2	C69011	conserved hypothetical	6.05e+01
36	34	94.4	1021	2	S44644	F37A4.7 protein - Cae	6.05e+01
37	34	94.4	3135	2	A48584	transmission-blocking	6.05e+01
38	33	91.7	146	5	1H7H	cyclic parathyroid ho	1.06e+02
39	33	91.7	146	1	HBOL	hemoglobin beta chain	1.06e+02
40	33	91.7	147	1	HBMS	hemoglobin beta major	1.06e+02
41	33	91.7	147	2	S34719	hemoglobin beta-2.0 c	1.06e+02
42	33	91.7	273	5	1ORDA	quinone-reductase (EC	1.06e+02
43	33	91.7	273	5	1ORDA	quinone-reductase (EC	1.06e+02
44	33	91.7	274	2	152851	NAD(P)H dehydrogenase	1.06e+02
45	33	91.7	578	2	E69259	aldehyde ferredoxin o	1.06e+02

ALIGNMENTS

RESULT	1	12WG	#type complete
ENTRY	parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -		
TITLE	synthetic		
ALTERNATE_NAMES	n-succinyl-hpgh(4-37)		
PDB_TITLE	succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM	#formal_name synthetic		
REFERENCE	A67743		
#authors	Roesch, P.; Marx, U.C.		
#submission	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WG		
REFERENCE	TN003319		
#authors	Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996		
COMMENT	Resolution: not applicable		
KEYWORDS	Determination: NMR		
FEATURE	disease mutation: hormone; signal		
2-9	#region helix (right hand alpha) \		
15-25	#region helix (right hand alpha)		
SUMMARY	#length 34 #molecular-weight 4128 #checksum 5508		
Query Match	100.0%; Score 36; DB 5; Length 34;		
Best Local Similarity	100.0%; Pred. No. 1.89e+01;		
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	6 HNLGK 10		
OY	1 HNLGK 5		
RESULT	2	12WF	#type complete
ENTRY	parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -		
TITLE	synthetic		
ALTERNATE_NAMES	n-acetyl-hpgh(4-37)		
PDB_TITLE	structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures		
ORGANISM	#formal_name synthetic		
REFERENCE	A67742		
#authors	Roesch, P.; Marx, U.C.		
#submission	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WF		
REFERENCE	TN003318		
#authors	Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loesung,		

COMMENT pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
 COMMENT Resolution: not applicable
 KEYWORDS Determination: NMR
 FEATURE disease mutation; hormone; signal
 3-6
 14-27
 SUMMARY #region helix (right hand alpha) \
 #region helix (right hand alpha) \
 #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 36; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.89e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 HNLGK 10
 1 HNLGK 5
 QY
 Search completed: Thu Jul 30 10:35:46 1998
 CPU time : 17 secs.

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:34:11 1998; Msrch time 2.00 Seconds
Tabular output not generated. 62.590 Million cell updates/sec

Title: >US-08-817-547A-17
Description: (1-5) from US08817547A.pep
Perfect Score: 36
Sequence: 1 HNLGK 5

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 18.208; Variance 13.355; scale 1.363

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	36	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	3.42e+00
2	36	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	3.42e+00
3	36	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	3.42e+00
4	36	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	3.42e+00
5	36	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.42e+00
6	36	100.0	894	1	KDPD_ECOLI SENSOR PROTEIN KDPD (E	3.42e+00
7	36	100.0	1063	1	DPOK_CICAP PROBABLE DNA POLYMERAS	3.42e+00
8	36	100.0	1209	1	THR_DROME THREE ROWS PROTEIN..	3.42e+00
9	36	100.0	146	1	HHB_ONDZI HEMOGLOBIN BETA CHAIN.	1.41e+01
10	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
11	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
12	36	100.0	229	1	NEF_STVAG NEGATIVE FACTOR (F-PRO	1.41e+01
13	36	100.0	412	1	CCA_ECOLI TRNA NUCLEOTIDYLTRANSF	1.41e+01
14	36	100.0	416	1	CCA_HAEIN TRNA NUCLEOTIDYLTRANSF	1.41e+01
15	36	100.0	455	1	YSCP_YERPS YOP PROTEINS TRANSLOC	1.41e+01
16	36	100.0	573	1	P60_HUMAN MITOCHONDRIAL MATRIX P	1.41e+01
17	36	100.0	573	1	P60_RAT MITOCHONDRIAL MATRIX P	1.41e+01
18	36	100.0	573	1	P60_MOUSE MITOCHONDRIAL MATRIX P	1.41e+01
19	36	100.0	573	1	P60_CRIGR MITOCHONDRIAL MATRIX P	1.41e+01
20	36	100.0	711	1	YOPF_BACSU HYPOTHETICAL 79.2 KD P	1.41e+01
21	36	100.0	1021	1	YPT7_CAELI HYPOTHETICAL 111.7 KD	1.41e+01
22	36	100.0	3135	1	S230_PLAFO TRANSMISSION-BLOCKING	1.41e+01
23	36	100.0	146	1	HHB_SPEPTO HEMOGLOBIN BETA-S AND	2.78e+01

24	33	91.7	146	1	HHB2_RAT HEMOGLOBIN BETA CHAIN.	2.78e+01
25	33	91.7	146	1	HHB2_MITCA HEMOGLOBIN BETA CHAIN.	2.78e+01
26	33	91.7	146	1	HHB2_SPECI HEMOGLOBIN BETA CHAIN.	2.78e+01
27	33	91.7	146	1	HHB1_RAT HEMOGLOBIN BETA CHAIN.	2.78e+01
28	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
29	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA CHAIN.	2.78e+01
30	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA CHAIN.	2.78e+01
31	33	91.7	235	1	REPAT_CSV REPEAT ELEMENT PROTEIN	2.78e+01
32	33	91.7	273	1	DHOU_MOUSE NAD(P)H DEHYDROGENASE	2.78e+01
33	33	91.7	273	1	DHOU_MOUSE NAD(P)H DEHYDROGENASE	2.78e+01
34	33	91.7	274	1	DHOU_MOUSE NAD(P)H DEHYDROGENASE	2.78e+01
35	33	91.7	409	1	TRPB_METVO TRYPTOPHAN SYNTHASE BE	2.78e+01
36	33	91.7	506	1	CPB1_CANFA CYTOCHROME P450 L1B1	2.78e+01
37	33	91.7	787	1	DPOL_HPBDC DNA POLYMERASE (EC 2.7	2.78e+01
38	33	91.7	788	1	DPOL_HPBDC DNA POLYMERASE (EC 2.7	2.78e+01
39	33	91.7	788	1	DPOL_HPBDC DNA POLYMERASE (EC 2.7	2.78e+01
40	33	91.7	797	1	DPOL_HPBDC PROBABLE DNA POLYMERAS	2.78e+01
41	33	91.7	836	1	DPOL_HPBDC DNA POLYMERASE (EC 2.7	2.78e+01
42	33	91.7	972	1	AND_BOVIN PEPTIDYL-GLYCINE ALPHA	2.78e+01
43	33	91.7	974	1	AND_BOVIN PEPTIDYL-GLYCINE ALPHA	2.78e+01
44	33	91.7	976	1	AND_RAT PEPTIDYL-GLYCINE ALPHA	2.78e+01
45	33	91.7	979	1	AND_MOUSE PEPTIDYL-GLYCINE ALPHA	2.78e+01

ALIGNMENTS

RESULT	ID	PTHY_BOVIN	STANDARD;	PTH;	115 AA.
AC	P01268;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; ARTIODACTYLA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE: 80056617.				
RA	KRONENBERG H.M., MCDEVITT B.E., MAZCOUB J.A., NATHANS J., SHARP P.A.,				
RA	POTTS J.T. JR., RICH A.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE: 82037785.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE: 83105964.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE: 84262483.				
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;				
RL	GENE 28:319-329(1984).				
RN	[5]				
RP	SEQUENCE OF 26-115.				
RA	MEDLINE: 7412666.				
RA	HAMILTON J.W., NATL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,				
RL	COHN D.V.;				
RN	[6]				
RP	SEQUENCE OF 32-115.				
RA	MEDLINE: 71076162.				
RA	NATL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,				
RL	AURBACH G.D., POTTS J.T. JR.;				
RN	[7]				
RP	HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).				
RL	SEQUENCE OF 32-115.				
RA	MEDLINE: 71063634.				

RA BREWER H.B. JR., RONAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
 DEFLOS L.J., DAWSON B.F., HOGAN M.L., AUBACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL; V00106; G85; -;
 DR EMBL; J00023; G163641; -;
 DR EMBL; J00024; G163643; -;
 DR EMBL; J00024; E18249; ALT_SEQ.
 DR EMBL; J00024; E18250; ALT_INIT.
 DR EMBL; K01938; G163647; -;
 DR EMBL; M25082; G163645; -;
 DR PIR; A01534; PTBO.
 DR PIR; A24949; A24949.
 DR PROSITE; PS00335; PARATHYROID; 1.
 SIGNAL
 FT PROPER 1 25
 FT CHAIN 26 31
 FT CONFLICT 32 115 PARATHYROID HORMONE.
 V -> G (IN REF. 4).
 SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;

Query Match 100.0%; Score 36; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 3,42e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGR 44
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 QY 1 HNLGR 5

RESULT 2
 ID PTH_PIG STANDARD; PRT; 115 AA.
 AC P01269;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; ARTIODACTYLA.
 RN [1]
 NA SEQUENCE FROM N.A.
 SCHMELZER H.-J., GROSS G., WIDERA G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN [2]
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN [3]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 74253317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 POTTS J.T. JR.;
 RL BIOCHEMISTRY 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL; X05722; G1839; -;
 DR PIR; B26806; B26806.
 DR PIR; B26806; B26806.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPER 26 31
 FT CHAIN 32 115 PARATHYROID HORMONE.

SQ SEQUENCE 115 AA; 12852 MM; 98B67FA7 CRC32;

Query Match 100.0%; Score 36; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 3,42e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGR 44
 |||||
 QY 1 HNLGR 5

Search completed: Thu Jul 30 10:34:18 1998
 Job time : 7 secs.

RL MOL. MICROBIOL. 22:175-191(1996).
 DR EMBL: Y08257; E283828;
 SQ SEQUENCE 123 AA; 14021 MW; 316E0391 CRC32;
 Query Match 100.0%; Score 36; DB 9; Length 123;
 Best Local Similarity 100.0%; Pred. No. 5.59e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 HNLGK 10
 QY 1 HNLGK 5

Search completed: Thu Jul 30 10:35:11 1998
 Job time : 34 secs.

SQ Sequence 38 AA:

Query Match 100.0%; Score 103; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.80e-03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLGQVHNFVAL 37
 |||
 QY 1 LKKLGQVHNFVAL 14

RESULT 2

ID R58151 standard; peptide; 38 AA.
 AC R58151;
 DT 20-SEP-1994 (first entry)
 DE [Ser22]-hPTH(1-38)-OH.
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 Synthetic.
 GR269176-A.
 02-FEB-1994.
 PF 12-JUL-1993; 014384.
 PR 15-JUL-1992; GB-015009.
 PR 18-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 23-DEC-1992; GB-026861.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERINDINGEN VERW GES MBH.
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 DR WPI; 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 PS Example 148; Page 40; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SO Sequence 38 AA;

Query Match 100.0%; Score 103; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.80e-03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLGQVHNFVAL 37
 |||
 QY 1 LKKLGQVHNFVAL 14

Search completed: Thu Jul 30 10:39:16 1998
 Job time : 24 secs.

MIRCH

(TM)

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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:38:07 1998; MasPar time 3.41 Seconds
150.175 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-18
Description: (1-14) from US08817547A.pep
Perfect Score: 103
Sequence: 1 LRKKLDVHNFEVAL 14

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 26.838; Variance 43.748; scale 0.613

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	103	100.0	34	5	12WE parathyroid hormone (8.54e-08	
2	103	100.0	34	5	12WG parathyroid hormone (8.54e-08	
3	103	100.0	34	5	12WF parathyroid hormone (8.54e-08	
4	103	100.0	35	5	12MD parathyroid hormone (8.54e-08	
5	103	100.0	36	5	12WB parathyroid hormone (8.54e-08	
6	103	100.0	37	5	12WC parathyroid hormone (8.54e-08	
7	103	100.0	37	5	12WH parathyroid hormone (8.54e-08	
8	103	100.0	115	1	PTHU parathyroid hormone (8.54e-08	
9	103	100.0	115	2	JC4202 parathyroid hormone (8.54e-08	
10	103	100.0	115	1	PRPG parathyroid hormone (8.54e-08	
11	103	100.0	115	1	PTBO parathyroid hormone (8.54e-08	
12	101	98.1	115	2	A05091 parathyroid hormone (2.16e-07	
13	91	88.3	105	2	151851 parathyroid hormone (2.06e-05	
14	84	81.6	34	5	12HT cyclic parathyroid hormone (4.52e-04	
15	84	81.6	34	5	12WA parathyroid hormone (4.52e-04	
16	66	64.1	2475	2	S35307 polypeptide pp220 pre (7.59e-01	
17	64	62.1	444	2	S09681 citrate transport pro (1.64e-00	
18	61	59.2	462	2	A42401 macrophage elastase (5.05e+00	
19	58	56.3	183	2	S42547 glucose-1-phosphate a (1.51e+01	
20	58	56.3	313	1	QOECIL hypothetical 34.6K pr (1.51e+01	
21	58	56.3	330	1	151545 myc protein - African (1.51e+01	
22	58	56.3	419	1	TVXIMC transforming protein (1.51e+01	
23	58	56.3	2843	1	R8HUP adenomatous polyposis (1.51e+01	

24	58	56.3	2845	2	149505	adenomatous polyposis (1.51e+01
25 <td>57</td> <td>55.3</td> <td>281</td> <td>2</td> <td>S41854 phosphoprotein phosph (2.15e+01</td>	57	55.3	281	2	S41854 phosphoprotein phosph (2.15e+01	
26 <td>57</td> <td>55.3</td> <td>470</td> <td>2</td> <td>A49499 metalloelastase HME (2.15e+01</td>	57	55.3	470	2	A49499 metalloelastase HME (2.15e+01	
27 <td>57</td> <td>55.3</td> <td>525</td> <td>2</td> <td>C64313 hypothetical protein (2.15e+01</td>	57	55.3	525	2	C64313 hypothetical protein (2.15e+01	
28 <td>57</td> <td>55.3</td> <td>555</td> <td>2</td> <td>S69641 hypothetical protein (2.15e+01</td>	57	55.3	555	2	S69641 hypothetical protein (2.15e+01	
29 <td>56<td>54.4</td><td>208</td><td>2</td><td>S20583 DNA-directed RNA poly (3.06e+01</td></td>	56 <td>54.4</td> <td>208</td> <td>2</td> <td>S20583 DNA-directed RNA poly (3.06e+01</td>	54.4	208	2	S20583 DNA-directed RNA poly (3.06e+01	
30 <td>56<td>54.4</td><td>445</td><td>2</td><td>S43452 surface antigen - hep (3.06e+01</td></td>	56 <td>54.4</td> <td>445</td> <td>2</td> <td>S43452 surface antigen - hep (3.06e+01</td>	54.4	445	2	S43452 surface antigen - hep (3.06e+01	
31 <td>56<td>54.4</td><td>475</td><td>1</td><td>KCRITR stromelysin I (EC 3.4 (3.06e+01</td></td>	56 <td>54.4</td> <td>475</td> <td>1</td> <td>KCRITR stromelysin I (EC 3.4 (3.06e+01</td>	54.4	475	1	KCRITR stromelysin I (EC 3.4 (3.06e+01	
32 <td>56<td>54.4</td><td>477</td><td>1</td><td>KCMS61 stromelysin I (EC 3.4 (3.06e+01</td></td>	56 <td>54.4</td> <td>477</td> <td>1</td> <td>KCMS61 stromelysin I (EC 3.4 (3.06e+01</td>	54.4	477	1	KCMS61 stromelysin I (EC 3.4 (3.06e+01	
33 <td>56<td>54.4</td><td>478</td><td>1</td><td>KCRBS1 stromelysin I (EC 3.4 (3.06e+01</td></td>	56 <td>54.4</td> <td>478</td> <td>1</td> <td>KCRBS1 stromelysin I (EC 3.4 (3.06e+01</td>	54.4	478	1	KCRBS1 stromelysin I (EC 3.4 (3.06e+01	
34 <td>56<td>54.4</td><td>608</td><td>2</td><td>A46312 gag polyprotein - hum (3.06e+01</td></td>	56 <td>54.4</td> <td>608</td> <td>2</td> <td>A46312 gag polyprotein - hum (3.06e+01</td>	54.4	608	2	A46312 gag polyprotein - hum (3.06e+01	
35 <td>56<td>54.4</td><td>651</td><td>2</td><td>G64058 DNA topoisomerase (EC (3.06e+01</td></td>	56 <td>54.4</td> <td>651</td> <td>2</td> <td>G64058 DNA topoisomerase (EC (3.06e+01</td>	54.4	651	2	G64058 DNA topoisomerase (EC (3.06e+01	
36 <td>56<td>54.4</td><td>752</td><td>1</td><td>C2HU complement C2 precurs (3.06e+01</td></td>	56 <td>54.4</td> <td>752</td> <td>1</td> <td>C2HU complement C2 precurs (3.06e+01</td>	54.4	752	1	C2HU complement C2 precurs (3.06e+01	
37 <td>55<td>53.4</td><td>102</td><td>2</td><td>S53076 probable membrane pro (4.33e+01</td></td>	55 <td>53.4</td> <td>102</td> <td>2</td> <td>S53076 probable membrane pro (4.33e+01</td>	53.4	102	2	S53076 probable membrane pro (4.33e+01	
38 <td>55<td>53.4</td><td>119</td><td>2</td><td>A34937 parathyroid hormone p (4.33e+01</td></td>	55 <td>53.4</td> <td>119</td> <td>2</td> <td>A34937 parathyroid hormone p (4.33e+01</td>	53.4	119	2	A34937 parathyroid hormone p (4.33e+01	
39 <td>55<td>53.4</td><td>203</td><td>2</td><td>S20584 DNA-directed RNA poly (4.33e+01</td></td>	55 <td>53.4</td> <td>203</td> <td>2</td> <td>S20584 DNA-directed RNA poly (4.33e+01</td>	53.4	203	2	S20584 DNA-directed RNA poly (4.33e+01	
40 <td>55<td>53.4</td><td>227</td><td>2</td><td>A24911 prolactin-like protei (4.33e+01</td></td>	55 <td>53.4</td> <td>227</td> <td>2</td> <td>A24911 prolactin-like protei (4.33e+01</td>	53.4	227	2	A24911 prolactin-like protei (4.33e+01	
41 <td>55<td>53.4</td><td>284</td><td>2</td><td>S74516 dimethyladenosine tra (4.33e+01</td></td>	55 <td>53.4</td> <td>284</td> <td>2</td> <td>S74516 dimethyladenosine tra (4.33e+01</td>	53.4	284	2	S74516 dimethyladenosine tra (4.33e+01	
42 <td>55<td>53.4</td><td>453</td><td>2</td><td>S59456 hypothetical protein (4.33e+01</td></td>	55 <td>53.4</td> <td>453</td> <td>2</td> <td>S59456 hypothetical protein (4.33e+01</td>	53.4	453	2	S59456 hypothetical protein (4.33e+01	
43 <td>55<td>53.4</td><td>692</td><td>2</td><td>A34548 foliitropin receptor (4.33e+01</td></td>	55 <td>53.4</td> <td>692</td> <td>2</td> <td>A34548 foliitropin receptor (4.33e+01</td>	53.4	692	2	A34548 foliitropin receptor (4.33e+01	
44 <td>55<td>53.4</td><td>911</td><td>2</td><td>S28098 ste6 protein - fission (4.33e+01</td></td>	55 <td>53.4</td> <td>911</td> <td>2</td> <td>S28098 ste6 protein - fission (4.33e+01</td>	53.4	911	2	S28098 ste6 protein - fission (4.33e+01	
45 <td>55<td>53.4</td><td>1634</td><td>2</td><td>JC5500 phosphoinositide 3-ki (4.33e+01</td></td>	55 <td>53.4</td> <td>1634</td> <td>2</td> <td>JC5500 phosphoinositide 3-ki (4.33e+01</td>	53.4	1634	2	JC5500 phosphoinositide 3-ki (4.33e+01	

ALIGNMENTS

RESULT	ENTRY	1	12WE	#type complete
TITLE			parathyroid hormone (residues 4-37) - human	
ALTERNATE_NAMES			HPTH(4-37)	
PDB_TITLE			structure of human parathyroid hormone fragment 4-37, NMR 10 structures	
ORGANISM			.#formal_name Homo sapiens #common_name man	
REFERENCE			A67860 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996	
#authors				
#submission				
#cross-references			PDB:12WE	
REFERENCE			TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
#book				
COMMENT			Resolution: not applicable	
COMMENT			Determination: NMR	
KEYWORDS			hormone	
FEATURE				
15-25			#region helix (right hand alpha)	
SUMMARY			#length 34 #molecular-weight 4128 #checksum 5508	
Query Match			100.0%; Score 103; DB 5; Length 34;	
Best Local Similarity			100.0%; Pred. No. 8.54e-08;	
Matches			14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	21	LRKKLDVHNFEVAL 34		
QY	1	LRKKLDVHNFEVAL 14		
RESULT	2	12WG	#type complete	
ENTRY			parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -	
TITLE			synthetic	
ALTERNATE_NAMES			n-succinyl-hPTH(4-37)	
PDB_TITLE			succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM			.#formal_name synthetic	
REFERENCE			A67743 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996	
#authors				
#submission				
#cross-references			PDB:12WG	
REFERENCE			TN003319 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
#book				
COMMENT			Resolution: not applicable	

```







COMMENT      Determination: NMR
KEYWORDS     disease mutation; hormone; signal
FEATURE      2-9      #region helix (right hand alpha)\
                15-25  #region helix (right hand alpha)
SUMMARY      #length 34 #molecular-weight 4128 #checksum 5508

Query Match  100.0%; Score 103; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. NO. 8.54e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LKKKLDVHNFFVAL 34
QY 1 LKKKLDVHNFFVAL 14

Search completed: Thu Jul 30 10:38:34 1998
Job time : 27 secs.

```

M105E161
(TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:37:03 1998; Maspar time 4.02 Seconds
146.589 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-18
Description: (1-14) from US08817547A.pep
Perfect Score: 103
Sequence: 1 LRRKLDVHNFVAL 14

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 26.844; Variance 35.900; scale 0.748

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	91	88.3	105 10	063473	PARATHYROID HORMONE (F	3.26e-07
2	66	64.1	2475 11	008358	POLYPROTEIN PP220.	1.09e-01
3	61	59.2	207 11	038628	ORE36L.	1.07e+00
4	61	59.2	342 11	038474	SIMILAR TO BACTERIOPHA	1.07e+00
5	59	57.3	320 9	005914	HYPOTHEICAL PROTEIN I	2.57e+00
6	58	56.3	228 3	001841	COSMID F56F4.	3.97e+00
7	58	56.3	330 12	091794	MYC PROTEIN (FRAGMENT	3.97e+00
8	58	56.3	591 3	094367	F52E10.5 (FRAGMENT)	3.97e+00
9	58	56.3	1291 2	015047	MRNA (K1A0067) FOR OR	3.87e+00
10	58	56.3	2743 3	015162	POLYPOSIS LOCUS-ENCODE	3.97e+00
11	58	56.3	2829 12	P70039	ADENOMATOUS POLYPOSIS	3.97e+00
12	58	56.3	2842 10	P70478	APC PROTEIN.	3.97e+00
13	58	56.3	2844 2	015163	POLYPOSIS LOCUS-ENCODE	3.97e+00
14	58	56.3	2845 10	061315	ADENOMATOUS POLYPOSIS	3.97e+00
15	57	55.3	299 3	019742	SIMILAR TO SER/THR PRO	6.09e+00
16	57	55.3	535 1	003359	D8035.17P.	6.09e+00
17	57	55.3	688 10	064183	FOLICICLE-STIMULATING H	6.09e+00
18	56	54.4	1077 8	P92974	UBIQUITIN-ACTIVATING E	9.30e+00
19	56	54.4	445 11	067953	PRE-S-S ORF.	9.30e+00
20	56	54.4	477 4	Q28397	MATRIX METALLOPROTEIN	9.30e+00

RESULT	ID	PRELIMINARY	PRT	105 AA.
21	56	54.4	752 2	013904
22	56	54.4	1080 8	P93393
23	55	53.4	231 1	005436
24	55	53.4	245 8	Q40969
25	55	53.4	265 8	Q39296
26	55	53.4	284 9	P72666
27	55	53.4	395 3	018530
28	55	53.4	453 1	004934
29	55	53.4	693 12	Q90719
30	55	53.4	821 9	Q31210
31	55	53.4	1167 10	063681
32	55	53.4	1186 10	008961
33	55	53.4	1459 3	Q21874
34	55	53.4	1634 2	Q00750
35	55	53.4	2401 3	Q26216
36	55	53.4	2708 3	Q15791
37	55	53.4	2742 3	Q15801
38	55	53.4	2819 3	Q15792
39	54	52.4	465 10	Q63341
40	54	52.4	694 3	Q21225
41	54	52.4	735 3	Q17750
42	54	52.4	962 9	P95235
43	54	52.4	993 3	Q17162
44	54	52.4	344 11	P90213
45	54	52.4	4162 12	Q98918

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	063473;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATUUS NORVEGICUS (RAT).			
OC	EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-THYROID, AND PARATHYROID;			
RA	SCHMELZER H.J., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -			
FT	NONTER 1			
SO	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;			

Query Match 88.3%; Score 91; DB 10; Length 105;
Best Local Similarity 85.7%; Pred. No. 3.26e-07;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB	45	LRRKLDVHNFVAL 58
QY	1	LRRKLDVHNFVAL 14

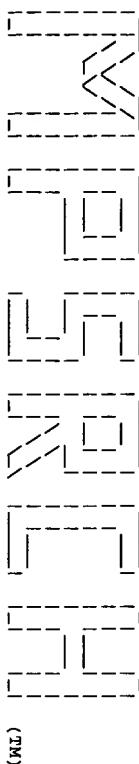
RESULT 2
ID 008358
AC 008358; PRELIMINARY; PRT; 2475 AA.
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE POLYPROTEIN PP220.
GN CP2475L.
OS AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).
OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93327788.
RA SIMON-MATEO C.; ANDRES G.; VINUELA E.;
RL EMBL J. 12:2977-2987(1993).

RN [2]
RP COMPLETE GENOME.
RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA RODRIGUEZ J.F., VINUELA E.,
RL VIROLOGY 208:249-278(1995).
CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
CC PROTEINS P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.
DR EMBL: Z22277; G394709; -;
DR EMBL: U18466; G780461; -;
KW POLYPROTEIN.
SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3C0A CRC32;

Query Match 64.1%; Score 66; DB 11; Length 2475;
Best local Similarity 75.0%; Pred. No. 1.09e-01;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1944 LRKTLQDVISFY 1955
||| ||| :||
QY 1 LRKRLQDVHNFV 12

Match completed: Thu Jul 30 10:37:48 1998
Job time : 45 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:41:57 1998; MasPar time 2.73 Seconds
Tabular output not generated. 73.134 Million cell updates/sec

Title: >US-08-817-547A-19
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 RKKIQDVHNFVAL 13

Scoring table:
PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.828; Variance 67.821; scale 0.278

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	95	100.0	38	9	R58123	[Ser19]-hPTH(1-38)-OH	1.55e-02
2	95	100.0	38	9	R58134	[Ile19]-hPTH(1-38)-OH	1.55e-02
3	95	100.0	38	9	R58018	Isopropyl-Llys(IsoPro	1.55e-02
4	95	100.0	38	9	R58138	[Ala21]-hPTH(1-38)-OH	1.55e-02
5	95	100.0	38	9	R58137	[Phe20]-hPTH(1-38)-OH	1.55e-02
6	95	100.0	38	9	R58124	[Lys19]-hPTH(1-38)-OH	1.55e-02
7	95	100.0	44	26	P30015	Human parathyroid hor	1.55e-02
8	95	100.0	47	25	W21946	Fusion protein compri	1.55e-02
9	95	100.0	84	27	W25687	Human parathyroid hor	1.55e-02
10	95	100.0	84	4	R23500	Porcine parathyroid h	1.55e-02
11	95	100.0	84	4	R23540	Bovine parathyroid ho	1.55e-02
12	95	100.0	84	4	R23387	Porcine parathyroid h	1.55e-02
13	95	100.0	84	4	R23262	Bovine parathyroid ho	1.55e-02
14	95	100.0	84	4	R21188	Human parathyroid hor	1.55e-02
15	95	100.0	84	4	R21189	Human parathyroid hor	1.55e-02
16	95	100.0	84	4	R23415	Porcine parathyroid h	1.55e-02
17	95	100.0	84	4	R23317	Bovine parathyroid ho	1.55e-02
18	95	100.0	84	4	R23429	Porcine parathyroid h	1.55e-02
19	95	100.0	84	4	R23359	Bovine parathyroid ho	1.55e-02

20	95	100.0	84	4	R23384	Porcine parathyroid h	1.55e-02
21	95	100.0	84	4	R23246	Human parathyroid hor	1.55e-02
22	95	100.0	84	4	R21184	Human parathyroid hor	1.55e-02
23	95	100.0	84	4	R21156	Human parathyroid hor	1.55e-02
24	95	100.0	84	4	R21157	Human parathyroid hor	1.55e-02
25	95	100.0	84	4	R23242	Human parathyroid hor	1.55e-02
26	95	100.0	84	4	R21240	Human parathyroid hor	1.55e-02
27	95	100.0	84	25	W29420	Human parathyroid hor	1.55e-02
28	95	100.0	84	4	R21169	Human parathyroid hor	1.55e-02
29	95	100.0	84	4	R23241	Human parathyroid hor	1.55e-02
30	95	100.0	84	4	R23501	Porcine parathyroid h	1.55e-02
31	95	100.0	84	4	R23237	Human parathyroid hor	1.55e-02
32	95	100.0	84	4	R21192	Human parathyroid hor	1.55e-02
33	95	100.0	84	4	R21164	Human parathyroid hor	1.55e-02
34	95	100.0	84	4	R21227	Human parathyroid hor	1.55e-02
35	95	100.0	84	4	R23258	Bovine parathyroid ho	1.55e-02
36	95	100.0	84	4	R21168	Bovine parathyroid hor	1.55e-02
37	95	100.0	84	4	R23290	Bovine parathyroid ho	1.55e-02
38	95	100.0	84	4	R23402	Porcine parathyroid h	1.55e-02
39	95	100.0	84	4	R23275	Bovine parathyroid ho	1.55e-02
40	95	100.0	84	4	R23394	Porcine parathyroid h	1.55e-02
41	95	100.0	84	4	R23326	Bovine parathyroid ho	1.55e-02
42	95	100.0	84	7	R34452	Bovine parathyroid ho	1.55e-02
43	95	100.0	84	4	R21211	Human parathyroid hor	1.55e-02
44	95	100.0	84	4	R23449	Porcine parathyroid h	1.55e-02
45	95	100.0	115	2	P80275	Sequence of human pre	1.55e-02

ALIGNMENTS

RESULT 1
ID R58123 standard; peptide; 38 AA.
AC R58123;
DT 20-SEP-1994 (first entry)
DE [Ser19]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PI 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026815.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 120; Page 39; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SO Sequence 38 AA.

Query Match 100.0%; Score 95; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.55e-02;
Matches 13; Conservatively 0; Mismatches 0; Indels 0; Gaps 0;
Db 25 rkkldqvhmfval 37

QY 1 RKKLDVHNFVAL 13

RESULT

2

ID R58134 standard; peptide; 38 AA.
AC R58134:
DT 20-SEP-1994 (first entry)
DE [Ile19]-hPTH(1-38)-OH.
KW human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PI (SANO) SANDOZ-ERFINDUNGEN VERW GRS MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
PI Waelchli R, Rainer A;
DR WPI; 94-018352/03
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 13i; Page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 95; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. NO. 1.55e-02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 25 rkkldgvhnfv al 37
1 RKKLDVHNFVAL 13

Search completed: Thu Jul 30 10:42:20 1998
Job time : 23 secs.

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NIPSEIN (TM)

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:41:13 1998; Maspar time 3.44 Seconds
Tabular output not generated. 138.161 Million cell updates/sec

Title: >US-08-817-547A-19
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 RKKLDVHNFFVAL 13

Scoring table: PAM 150
GAP 15

Searched: 120441 seqs, 36531193 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nrl3d

Statistics: Mean 25.919; Variance 39.318; scale 0.659

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	ID	Description	Pred. No.
1	95	100.0	34 5 12WE	parathyroid hormone (3.06e-07	
2	95	100.0	34 5 12WE	parathyroid hormone (3.06e-07	
3	95	100.0	34 5 12WE	parathyroid hormone (3.06e-07	
4	95	100.0	35 5 12WE	parathyroid hormone (3.06e-07	
5	95	100.0	36 5 12WE	parathyroid hormone (3.06e-07	
6	95	100.0	37 5 12WE	parathyroid hormone (3.06e-07	
7	95	100.0	37 5 12WE	parathyroid hormone (3.06e-07	
8	95	100.0	115 1 PTHU	parathyroid hormone (3.06e-07	
9	95	100.0	115 1 PTHU	parathyroid hormone (3.06e-07	
10	95	100.0	115 1 PTHU	parathyroid hormone (3.06e-07	
11	95	100.0	115 1 PTHU	parathyroid hormone (3.06e-07	
12	95	100.0	115 1 PTHU	parathyroid hormone (3.06e-07	
13	83	87.4	105 2 1S1851	parathyroid hormone (2.53e-03	
14	76	80.0	34 5 12WE	parathyroid hormone (3.06e-07	
15	76	80.0	34 5 12WE	parathyroid hormone (3.06e-07	
16	58	61.1	183 2 S42547	glucose-1-phosphate a 5.38e+00	
17	58	61.1	2475 2 S35307	polypeptide pp220 pre 7.35e+00	
18	57	60.0	555 2 S69641	hypothetical protein 1.17e+01	
19	56	58.9	281 2 S41854	hypothetical protein 1.17e+01	
20	56	58.9	444 2 S09681	citrate transport pro 1.17e+01	
21	56	58.9	475 1 KCRTH	stromelysin 1 (EC 3.4 1.17e+01	
22	56	58.9	477 1 KCMSS1	stromelysin 1 (EC 3.4 1.17e+01	
23	56	58.9	478 1 KCRBS1	stromelysin 1 (EC 3.4 1.17e+01	

24	56	58.9	651	2	G64068	DNA topoisomerase (EC 1.17e+01
25 <td>55<td>57.9<td>692<td>2<td>A34548<td>foliitropin receptor 1.71e+01</td></td></td></td></td></td>	55 <td>57.9<td>692<td>2<td>A34548<td>foliitropin receptor 1.71e+01</td></td></td></td></td>	57.9 <td>692<td>2<td>A34548<td>foliitropin receptor 1.71e+01</td></td></td></td>	692 <td>2<td>A34548<td>foliitropin receptor 1.71e+01</td></td></td>	2 <td>A34548<td>foliitropin receptor 1.71e+01</td></td>	A34548 <td>foliitropin receptor 1.71e+01</td>	foliitropin receptor 1.71e+01
26 <td>54<td>56.8<td>102<td>2<td>S53076<td>probable membrane pro 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>102<td>2<td>S53076<td>probable membrane pro 2.50e+01</td></td></td></td></td>	56.8 <td>102<td>2<td>S53076<td>probable membrane pro 2.50e+01</td></td></td></td>	102 <td>2<td>S53076<td>probable membrane pro 2.50e+01</td></td></td>	2 <td>S53076<td>probable membrane pro 2.50e+01</td></td>	S53076 <td>probable membrane pro 2.50e+01</td>	probable membrane pro 2.50e+01
27 <td>54<td>56.8<td>445<td>2<td>S43492<td>surface antigen - hep 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>445<td>2<td>S43492<td>surface antigen - hep 2.50e+01</td></td></td></td></td>	56.8 <td>445<td>2<td>S43492<td>surface antigen - hep 2.50e+01</td></td></td></td>	445 <td>2<td>S43492<td>surface antigen - hep 2.50e+01</td></td></td>	2 <td>S43492<td>surface antigen - hep 2.50e+01</td></td>	S43492 <td>surface antigen - hep 2.50e+01</td>	surface antigen - hep 2.50e+01
28 <td>54<td>56.8<td>525<td>2<td>G64313<td>hypothetical protein 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>525<td>2<td>G64313<td>hypothetical protein 2.50e+01</td></td></td></td></td>	56.8 <td>525<td>2<td>G64313<td>hypothetical protein 2.50e+01</td></td></td></td>	525 <td>2<td>G64313<td>hypothetical protein 2.50e+01</td></td></td>	2 <td>G64313<td>hypothetical protein 2.50e+01</td></td>	G64313 <td>hypothetical protein 2.50e+01</td>	hypothetical protein 2.50e+01
29 <td>54<td>56.8<td>608<td>2<td>A46312<td>gag polypeptide - hum 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>608<td>2<td>A46312<td>gag polypeptide - hum 2.50e+01</td></td></td></td></td>	56.8 <td>608<td>2<td>A46312<td>gag polypeptide - hum 2.50e+01</td></td></td></td>	608 <td>2<td>A46312<td>gag polypeptide - hum 2.50e+01</td></td></td>	2 <td>A46312<td>gag polypeptide - hum 2.50e+01</td></td>	A46312 <td>gag polypeptide - hum 2.50e+01</td>	gag polypeptide - hum 2.50e+01
30 <td>54<td>56.8<td>694<td>2<td>UC2237<td>foliitropin receptor 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>694<td>2<td>UC2237<td>foliitropin receptor 2.50e+01</td></td></td></td></td>	56.8 <td>694<td>2<td>UC2237<td>foliitropin receptor 2.50e+01</td></td></td></td>	694 <td>2<td>UC2237<td>foliitropin receptor 2.50e+01</td></td></td>	2 <td>UC2237<td>foliitropin receptor 2.50e+01</td></td>	UC2237 <td>foliitropin receptor 2.50e+01</td>	foliitropin receptor 2.50e+01
31 <td>54<td>56.8<td>752<td>2<td>S51866<td>HPR1 protein - yeast 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>752<td>2<td>S51866<td>HPR1 protein - yeast 2.50e+01</td></td></td></td></td>	56.8 <td>752<td>2<td>S51866<td>HPR1 protein - yeast 2.50e+01</td></td></td></td>	752 <td>2<td>S51866<td>HPR1 protein - yeast 2.50e+01</td></td></td>	2 <td>S51866<td>HPR1 protein - yeast 2.50e+01</td></td>	S51866 <td>HPR1 protein - yeast 2.50e+01</td>	HPR1 protein - yeast 2.50e+01
32 <td>54<td>56.8<td>1323<td>2<td>PN0568<td>connectin 3b - chick 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>1323<td>2<td>PN0568<td>connectin 3b - chick 2.50e+01</td></td></td></td></td>	56.8 <td>1323<td>2<td>PN0568<td>connectin 3b - chick 2.50e+01</td></td></td></td>	1323 <td>2<td>PN0568<td>connectin 3b - chick 2.50e+01</td></td></td>	2 <td>PN0568<td>connectin 3b - chick 2.50e+01</td></td>	PN0568 <td>connectin 3b - chick 2.50e+01</td>	connectin 3b - chick 2.50e+01
33 <td>54<td>56.8<td>3344<td>2<td>J01899<td>genome polypeptide - 2.50e+01</td></td></td></td></td></td>	54 <td>56.8<td>3344<td>2<td>J01899<td>genome polypeptide - 2.50e+01</td></td></td></td></td>	56.8 <td>3344<td>2<td>J01899<td>genome polypeptide - 2.50e+01</td></td></td></td>	3344 <td>2<td>J01899<td>genome polypeptide - 2.50e+01</td></td></td>	2 <td>J01899<td>genome polypeptide - 2.50e+01</td></td>	J01899 <td>genome polypeptide - 2.50e+01</td>	genome polypeptide - 2.50e+01
34 <td>53<td>55.8<td>449<td>2<td>S70651<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>449<td>2<td>S70651<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td>	55.8 <td>449<td>2<td>S70651<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td>	449 <td>2<td>S70651<td>leukotriene-A4 hydrol 3.62e+01</td></td></td>	2 <td>S70651<td>leukotriene-A4 hydrol 3.62e+01</td></td>	S70651 <td>leukotriene-A4 hydrol 3.62e+01</td>	leukotriene-A4 hydrol 3.62e+01
35 <td>53<td>55.8<td>145<td>5<td>1AT0<td>17-hedgehog 17-kda fr 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>145<td>5<td>1AT0<td>17-hedgehog 17-kda fr 3.62e+01</td></td></td></td></td>	55.8 <td>145<td>5<td>1AT0<td>17-hedgehog 17-kda fr 3.62e+01</td></td></td></td>	145 <td>5<td>1AT0<td>17-hedgehog 17-kda fr 3.62e+01</td></td></td>	5 <td>1AT0<td>17-hedgehog 17-kda fr 3.62e+01</td></td>	1AT0 <td>17-hedgehog 17-kda fr 3.62e+01</td>	17-hedgehog 17-kda fr 3.62e+01
36 <td>53<td>55.8<td>271<td>2<td>G64698<td>16S rRNA - Helicobact 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>271<td>2<td>G64698<td>16S rRNA - Helicobact 3.62e+01</td></td></td></td></td>	55.8 <td>271<td>2<td>G64698<td>16S rRNA - Helicobact 3.62e+01</td></td></td></td>	271 <td>2<td>G64698<td>16S rRNA - Helicobact 3.62e+01</td></td></td>	2 <td>G64698<td>16S rRNA - Helicobact 3.62e+01</td></td>	G64698 <td>16S rRNA - Helicobact 3.62e+01</td>	16S rRNA - Helicobact 3.62e+01
37 <td>53<td>55.8<td>462<td>2<td>A42401<td>macrophage elastase (3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>462<td>2<td>A42401<td>macrophage elastase (3.62e+01</td></td></td></td></td>	55.8 <td>462<td>2<td>A42401<td>macrophage elastase (3.62e+01</td></td></td></td>	462 <td>2<td>A42401<td>macrophage elastase (3.62e+01</td></td></td>	2 <td>A42401<td>macrophage elastase (3.62e+01</td></td>	A42401 <td>macrophage elastase (3.62e+01</td>	macrophage elastase (3.62e+01
38 <td>53<td>55.8<td>470<td>2<td>A49499<td>metalloelastase HME (3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>470<td>2<td>A49499<td>metalloelastase HME (3.62e+01</td></td></td></td></td>	55.8 <td>470<td>2<td>A49499<td>metalloelastase HME (3.62e+01</td></td></td></td>	470 <td>2<td>A49499<td>metalloelastase HME (3.62e+01</td></td></td>	2 <td>A49499<td>metalloelastase HME (3.62e+01</td></td>	A49499 <td>metalloelastase HME (3.62e+01</td>	metalloelastase HME (3.62e+01
39 <td>53<td>55.8<td>471<td>2<td>A46400<td>segment polarity prot 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>471<td>2<td>A46400<td>segment polarity prot 3.62e+01</td></td></td></td></td>	55.8 <td>471<td>2<td>A46400<td>segment polarity prot 3.62e+01</td></td></td></td>	471 <td>2<td>A46400<td>segment polarity prot 3.62e+01</td></td></td>	2 <td>A46400<td>segment polarity prot 3.62e+01</td></td>	A46400 <td>segment polarity prot 3.62e+01</td>	segment polarity prot 3.62e+01
40 <td>53<td>55.8<td>471<td>3<td>A43480<td>leukotriene gene hed 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>471<td>3<td>A43480<td>leukotriene gene hed 3.62e+01</td></td></td></td></td>	55.8 <td>471<td>3<td>A43480<td>leukotriene gene hed 3.62e+01</td></td></td></td>	471 <td>3<td>A43480<td>leukotriene gene hed 3.62e+01</td></td></td>	3 <td>A43480<td>leukotriene gene hed 3.62e+01</td></td>	A43480 <td>leukotriene gene hed 3.62e+01</td>	leukotriene gene hed 3.62e+01
41 <td>53<td>55.8<td>610<td>2<td>S20444<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>610<td>2<td>S20444<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td>	55.8 <td>610<td>2<td>S20444<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td>	610 <td>2<td>S20444<td>leukotriene-A4 hydrol 3.62e+01</td></td></td>	2 <td>S20444<td>leukotriene-A4 hydrol 3.62e+01</td></td>	S20444 <td>leukotriene-A4 hydrol 3.62e+01</td>	leukotriene-A4 hydrol 3.62e+01
42 <td>53<td>55.8<td>611<td>2<td>JN0065<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>611<td>2<td>JN0065<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td>	55.8 <td>611<td>2<td>JN0065<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td>	611 <td>2<td>JN0065<td>leukotriene-A4 hydrol 3.62e+01</td></td></td>	2 <td>JN0065<td>leukotriene-A4 hydrol 3.62e+01</td></td>	JN0065 <td>leukotriene-A4 hydrol 3.62e+01</td>	leukotriene-A4 hydrol 3.62e+01
43 <td>53<td>55.8<td>611<td>2<td>S65947<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>611<td>2<td>S65947<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td></td>	55.8 <td>611<td>2<td>S65947<td>leukotriene-A4 hydrol 3.62e+01</td></td></td></td>	611 <td>2<td>S65947<td>leukotriene-A4 hydrol 3.62e+01</td></td></td>	2 <td>S65947<td>leukotriene-A4 hydrol 3.62e+01</td></td>	S65947 <td>leukotriene-A4 hydrol 3.62e+01</td>	leukotriene-A4 hydrol 3.62e+01
44 <td>53<td>55.8<td>632<td>2<td>S73824<td>MG242 homolog H91.orf 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>632<td>2<td>S73824<td>MG242 homolog H91.orf 3.62e+01</td></td></td></td></td>	55.8 <td>632<td>2<td>S73824<td>MG242 homolog H91.orf 3.62e+01</td></td></td></td>	632 <td>2<td>S73824<td>MG242 homolog H91.orf 3.62e+01</td></td></td>	2 <td>S73824<td>MG242 homolog H91.orf 3.62e+01</td></td>	S73824 <td>MG242 homolog H91.orf 3.62e+01</td>	MG242 homolog H91.orf 3.62e+01
45 <td>53<td>55.8<td>1321<td>2<td>S27337<td>multidrug resistance 3.62e+01</td></td></td></td></td></td>	53 <td>55.8<td>1321<td>2<td>S27337<td>multidrug resistance 3.62e+01</td></td></td></td></td>	55.8 <td>1321<td>2<td>S27337<td>multidrug resistance 3.62e+01</td></td></td></td>	1321 <td>2<td>S27337<td>multidrug resistance 3.62e+01</td></td></td>	2 <td>S27337<td>multidrug resistance 3.62e+01</td></td>	S27337 <td>multidrug resistance 3.62e+01</td>	multidrug resistance 3.62e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY			
TITLE			parathyroid hormone (residues 4-37) - human
ALTERNATE_NAMES			HPTH(4-37)
PDB_TITLE			structure of human parathyroid hormone fragment 4-37, NMR 10
ORGANISM			Structure Homo sapiens #common_name man
REFERENCE			A67860
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WE
REFERENCE			TN001721
#authors			Marx, U.C.
COMMENT			In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0. Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT			Resolution: not applicable
KEYWORDS			hormone
FEATURE			
15-25			
SUMMARY			#region helix (right hand alpha)
			#length 34 #molecular-weight 4128 #checksum 5508
Query Match			100.0%; Score 95; DB 5; Length 34;
Best Local Similarity			100.0%; Pred. No. 3.06e-07;
Matches			13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	22	RKKLDVHNFFVAL 34	
Qy	1	RKKLDVHNFFVAL 13	
RESULT	2	12WE	#type complete
ENTRY			parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -
TITLE			synthetic
ALTERNATE_NAMES			n-succinyl-hPTH(4-37)
PDB_TITLE			succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM			formal_name synthetic
REFERENCE			A67743
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WE
REFERENCE			TN003319
#authors			Marx, U.C.
COMMENT			In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0. Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT			Resolution: not applicable

Thu Jul 30 13:38:01 1998

US-08-817-547A-19.rpr

Page 2

```
COMMENT      Determination: NMR
KEYWORDS      disease mutation; hormone; signal
FEATURE
  2-9
  15-25
SUMMARY
  #region helix (right hand alpha)\
  #region helix (right hand alpha)
  #length 34 #molecular-weight 4128 #checksum 5508
Query Match      100.0%; Score 95; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.06e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 22 RKKLDVHNEVAL 34
OY 1 RKKLDVHNEVAL 13
```

Search completed: Thu Jul 30 10:41:40 1998
Job time : 27 secs.

N O T E S
***** (TM)

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:39:34 1998; MasPar time 2.25 Seconds
Tabular output not generated. 145.141 Million cell updates/sec

Title: >US-08-817-547A-19
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 RKRLDPVHNFVAL 13

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 27.177; Variance 32.181; scale 0.844

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	95	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	8.93e-10
2	95	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	8.93e-10
3	95	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	8.93e-10
4	95	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	8.93e-10
5	93	97.9	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.05e-09
6	58	61.1	184	1	GLUC2_ARATH GLUTCOSE-1-PHOSPHATE AD	8.46e-01
7	56	55.9	281	1	PCZ1_YEAST PROTEIN PHOSPHATASE 2C	2.18e+00
8	56	58.9	444	1	CIT1_KLEPN CITRATE-PROTON SYMPORT	2.18e+00
9	56	58.9	475	1	STROMELYSIN-1 PRECURSOR	2.18e+00
10	56	58.9	477	1	COG3_MOUSE STROMELYSIN-1 PRECURSOR	2.18e+00
11	56	58.9	478	1	COG3_RABIT STROMELYSIN-1 PRECURSOR	2.18e+00
12	56	58.9	651	1	TOP3_HAEIN DNA TOPISOMERASE III	2.18e+00
13	55	57.9	692	1	FSHR_RAT FOLLICLE STIMULATING H	3.46e+00
14	55	57.9	693	1	FSHR_CHICK FOLLICLE STIMULATING H	3.46e+00
15	54	56.8	102	1	YMH8_YEAST FOLLEINS (LENS FIBER C	5.46e+00
16	54	56.8	130	1	Y107_METJA HYPOTHEICAL PROTEIN M	5.46e+00
17	54	56.8	525	1	FSHR_EOVAR FOLLICLE STIMULATING H	5.46e+00
18	54	56.8	687	1	FSHR_HORSE FOLLICLE STIMULATING H	5.46e+00
19	54	56.8	694	1	FSHR_HORSE FOLLICLE STIMULATING H	5.46e+00
20	54	56.8	752	1	HPRI_YEAST GENOME POLYPROTEIN (CO	5.46e+00
21	54	56.8	3444	1	COGM_MOUSE MACROPHAGE METALLOELAS	8.55e+00
22	53	55.8	462	1	COGM_MOUSE MACROPHAGE METALLOELAS	8.55e+00
23	53	55.8	470	1	COGM_HUMAN MACROPHAGE METALLOELAS	8.55e+00

ID	PTHY_CANFA	STANDARD	PRT	115 AA.		
24	53	55.8	471	1	HH_DROME HEDGEHOG PROTEIN PRECU	8.55e+00
25	53	55.8	609	1	LKHA_RAT LEUKOTRIENE A-4 HYDROL	8.55e+00
26	53	55.8	610	1	LKHA_HUMAN LEUKOTRIENE A-4 HYDROL	8.55e+00
27	53	55.8	610	1	LKHA_MOUSE LEUKOTRIENE A-4 HYDROL	8.55e+00
28	53	55.8	632	1	Y242_MYCPN HYPOTHEICAL PROTEIN M	8.55e+00
29	53	55.8	1321	1	MRL1_CABEL MULTIDRUG RESISTANCE P	8.55e+00
30	53	55.8	2133	1	FAB_PIG COAGULATION FACTOR VII	8.55e+00
31	52	54.7	189	1	YNOO_YEAST VERY HYPOTHEICAL 21.7	1.33e+01
32	52	54.7	476	1	COGX_RAT STROMELYSIN-2 PRECURSOR	1.33e+01
33	52	54.7	695	1	FSHR_BOVIN FOLLICLE STIMULATING H	1.33e+01
34	52	54.7	695	1	FSHR_SHEEP FOLLICLE STIMULATING H	1.33e+01
35	52	54.7	925	1	DEL_HUMAN PROTO-ONCOGENE DEL PRE	1.33e+01
36	51	53.7	119	1	RT13_ACAGA MITOCHONDRIAL RIBOSOMA	2.06e+01
37	51	53.7	200	1	Y10P_ECOLI HYPOTHEICAL 22.3 KD P	2.06e+01
38	51	53.7	227	1	PRRA_RAT PLACENTAL PROLACTIN-LI	2.06e+01
39	51	53.7	232	1	PM16_YEAST PROBABLE MITOCHONDRIAL	2.06e+01
40	51	53.7	476	1	COGX_HUMAN STROMELYSIN-2 PRECURSOR	2.06e+01
41	51	53.7	636	1	RPOC_CYAPA DNA-DIRECTED RNA POLYM	2.06e+01
42	51	53.7	695	1	FSHR_PIG FOLLICLE STIMULATING H	2.06e+01
43	51	53.7	1302	1	RRLP_BTV10 RNA-DIRECTED RNA POLYM	2.06e+01
44	51	53.7	1444	1	RRLP_RDV RNA-DIRECTED RNA POLYM	2.06e+01
45	50	52.6	419	1	MYC1_XENLA MYC I PROTO-ONCOGENE P	3.16e+01

ALIGNMENTS

RESULT	1	STANDARD	PRT	115 AA.
ID	PTHY_CANFA	STANDARD	PRT	115 AA.
AC	P52212			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUETHERIA; CARNIVORA.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PARATHYROID.			
RX	MEDLINE: 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RL	DEWILLE J.W., CAPEN C.C.;			
CC	GENE 160:241-243(1995).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL: U15662; G558916; -			
DR	PROSITE: PS00335; PARATHYROID; 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL	1	25	BY SIMILARITY.
FT	PROPEP	26	31	BY SIMILARITY.
FT	CHAIN	32	115	PARATHYROID HORMONE.
SO	SEQUENCE	115 AA; 12957 MW; 16DEDEBC CRC32;		
Query Match 100.0%; Score 95; DB 1; Length 115;				
Best Local Similarity 100.0%; Pred. No. 8.93e-10;				
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	56 RKRLDPVHNFVAL 68			
Qy	1 RKRLDPVHNFVAL 13			
RESULT 2				
ID	PTHY_BOVIN	STANDARD	PRT	115 AA.
AC	P01268			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	BOS TAURUS (BOVINE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

Search completed: Thu Jul 30 10:39:40 1998
Job time : 6 secs.

```

OC EUTHERIA: ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTS J.T., JR., RICH A.;
RM PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RL COHN D.V.;
RM PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAMSON B.F.,
RL AUBACH G.D., POTTS J.T., JR.;
RM HOPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREWER H.B., JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFOS L.O., DAMSON B.F., HOGAN M.L., AUBACH G.D.;
RM PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; V00106; G85; -.
DR EMBL; J00023; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K01938; G163647; -.
DR EMBL; M25082; G163645; -.
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
DR KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EAS5F2 CRC32;

Query Match 100.0%; Score 95; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8,93e-10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 56 RKKLDVHNFFVAL 68
QY 1 RKKLDVHNFFVAL 13

```

WIDEORBIT (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:39:58 1998; MasPer time 3.95 Seconds
Tabular output not generated. 138.577 Million cell updates/sec

Title: >US-08-817-547A-19
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 RKKLDVHNFVAL 13

Scoring table:
PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_prodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 25.965; Variance 32.081; scale 0.809

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	83	87.4	105	10	063473	PARATHYROID HORMONE (F	1.95e-06
2	61	64.2	207	11	038628	ORF36L	2.58e-01
3	60	63.2	342	11	098474	SIMILAR TO BACTERIOPHA	4.21e-01
4	58	61.1	2475	11	008358	POLYPROTEIN PP220.	1.10e+00
5	57	60.0	555	1	003359	D8035.17P.	1.77e+00
6	57	60.0	688	10	064183	FOLICLE-STIMULATING H	1.77e+00
7	56	58.9	477	4	028397	MATRIX METALLOPROTEIN	2.88e+00
8	55	57.9	693	12	090719	OVARIAN FOLLICLE-STIM	4.48e+00
9	55	57.9	1459	3	021874	ROSE10.5.	4.48e+00
10	54	56.8	445	11	067953	PRE S-S ORF.	7.06e+00
11	54	56.8	993	3	017162	VINCULIN.	7.06e+00
12	54	56.8	1002	11	085025	HC, P3 AND C1 PROTEINS	7.06e+00
13	54	56.8	1323	12	008476	CONNECTIN (TITIN) (FRA	7.06e+00
14	54	56.8	3344	11	P90213	PRSV YK POLYPROTEIN.	7.06e+00
15	54	56.8	4162	12	098818	CONNECTIN/TITIN (FRAGM	7.06e+00
16	53	55.8	269	3	019322	COSMID F10G.	1.11e+01
17	53	55.8	271	9	025972	16S rRNA (ADENOSINE-N6	1.11e+01
18	53	55.8	299	3	019742	SIMILAR TO SER/THR PRO	1.11e+01
19	53	55.8	709	3	015783	HYBRID HISTIDINE KINAS	1.11e+01
20	53	55.8	1321	3	021349	KOBER.9.	1.11e+01

21	53	55.8	1354	3	022669	ZK930.1.	1.11e+01
22	52	54.7	300	9	003658	LYS-TYPE BETA-LACTAM	1.72e+01
23	52	54.7	314	8	042657	ANNEXIN.	1.72e+01
24	52	54.7	345	9	P95793	STBA.	1.72e+01
25	52	54.7	354	9	P77171	FROM BASES 1485094 TO	1.72e+01
26	52	54.7	606	9	046606	HYD GAMMA.	1.72e+01
27	51	53.7	232	1	007216	URA1 CIP SYNTHETASE.	2.67e+01
28	51	53.7	320	9	005914	HYPOTHETICAL PROTEIN I	2.67e+01
29	51	53.7	591	3	094367	F52E10.5 (FRAGMENT).	2.67e+01
30	51	53.7	733	3	024250	TARAN PROTEIN PRECURS	2.67e+01
31	51	53.7	884	11	066658	DNA HELICASE-PRIMASE C	2.67e+01
32	51	53.7	1283	3	018824	SIMILAR TO MULTIDRUG-R	2.67e+01
33	51	53.7	1302	11	065734	CORE PROTEIN.	2.67e+01
34	51	53.7	1302	11	065741	RNA-DIRECTED RNA POLYM	2.67e+01
35	51	53.7	1302	11	065739	RNA-DIRECTED RNA POLYM	2.67e+01
36	51	53.7	1302	11	065740	RNA-DIRECTED RNA POLYM	2.67e+01
37	51	53.7	1444	11	098631	RNA-DEPENDENT RNA POLY	2.67e+01
38	51	53.7	1648	2	015058	MRNA (K1A0042) FOR OR	2.67e+01
39	50	52.6	214	3	025927	MAJOR MEROZOITE SURFAC	4.10e+01
40	50	52.6	214	3	025942	MAJOR MEROZOITE SURFAC	4.10e+01
41	50	52.6	330	12	091794	MYC PROTEIN (FRAGMENT)	4.10e+01
42	50	52.6	360	9	033405	HYDROGENASE SMALL SUBU	4.10e+01
43	50	52.6	402	12	042479	PEROXYLASE (EC 4.9	4.10e+01
44	50	52.6	483	12	098857	STROMELYSIN-1/2-A.	4.10e+01
45	50	52.6	2829	12	P70039	ADENOMATOUS POLYPOSIS	4.10e+01

ALIGNMENTS

RESULT ID	1	PRELIMINARY: PRT: 105 AA.
AC	063473	
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	PARATHYROID HORMONE (FRAGMENT).	
GN	PTH.	
OS	RATTUS NORVEGICUS (RAT).	
OC	EUTHEROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUHARCTA; RODENTIA.	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-THYROID, AND PARATHYROID;	
RA	SCHWELZER H.J., GROSS G., WAYER H.;	
RL	ADV. GENE TECHNOL. 21:228-229(1984).	
DR	EMBL; M54875; G601933; -.	
FT	NON-TER 1	
SEQ	SEQUENCE 105 AA: 11746 MW; 6AC3163E CRC32;	

Query Match	87.4%; Score 83; DB 10; Length 105;
Best local Similarity	84.6%; Pred. No. 1.95e-06;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
DB	46 RKKLDVHNFVAL 58
OY	1 RKKLDVHNFVAL 13

RESULT ID	2	PRELIMINARY: PRT: 207 AA.
AC	038628	
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	ORF36L.	
OS	CYDIA POMONELLA GRANULOVIRUS.	
OC	VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS.	
GN	[1]	
RP	SEQUENCE FROM N.A.	
RA	JEHL J.A., VAN DER LINDEN I.F.A., VLAK J.M.;	
RL	VIRUS RES. 0:0-0(1997).	
DR	EMBL; AF002732; G2232189; -.	
SEQ	SEQUENCE 207 AA: 23915 MW; D2F05988 CRC32;	

Query Match 64.2%; Score 61; DB 11; Length 207;
Best Local Similarity 66.7%; Pred. No. 2.58e-01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 144 RLOEVHDFV 152
QY 3 KLDVHNFV 11

Search completed: Thu Jul 30 10:40:55 1998
Job time : 57 secs.

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:44:34 1998; MasPar time 2.69 Seconds
68.390 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A. pep
Perfect Score: 86
Sequence: 1 KKLQDVHNFVAL 12

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.088; Variance 63.020; scale 0.287

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	86	100.0	38	9	R58024 [Ala1, Ile2]-hPTH(1-38	6.03e-02
2	86	100.0	44	26	P30015 Human parathyroid hor	6.03e-02
3	86	100.0	47	25	W21946 Fusion protein compri	6.03e-02
4	86	100.0	84	27	W25687 Human parathyroid hor	6.03e-02
5	86	100.0	84	4	R23542 Bovine parathyroid ho	6.03e-02
6	86	100.0	84	4	R23471 Porcine parathyroid h	6.03e-02
7	86	100.0	84	4	R23387 Porcine parathyroid h	6.03e-02
8	86	100.0	84	4	R23262 Bovine parathyroid ho	6.03e-02
9	86	100.0	84	4	R23316 Bovine parathyroid ho	6.03e-02
10	86	100.0	84	4	R23346 Bovine parathyroid ho	6.03e-02
11	86	100.0	84	4	R23336 Bovine parathyroid ho	6.03e-02
12	86	100.0	84	4	R23429 Porcine parathyroid h	6.03e-02
13	86	100.0	84	4	R23259 Bovine parathyroid ho	6.03e-02
14	86	100.0	84	4	R23436 Porcine parathyroid h	6.03e-02
15	86	100.0	84	4	R23512 Bovine parathyroid hor	6.03e-02
16	86	100.0	84	4	R21157 Human parathyroid hor	6.03e-02
17	86	100.0	84	4	R21156 Human parathyroid hor	6.03e-02
18	86	100.0	84	4	R21185 Human parathyroid hor	6.03e-02
19	86	100.0	84	4	R21184 Human parathyroid hor	6.03e-02

20	86	100.0	84	4	R23371 Bovine parathyroid ho	6.03e-02
21	86	100.0	84	4	R23370 Bovine parathyroid ho	6.03e-02
22	86	100.0	84	25	W29420 Human parathyroid hor	6.03e-02
23	86	100.0	84	4	R21169 Human parathyroid hor	6.03e-02
24	86	100.0	84	4	R21170 Human parathyroid hor	6.03e-02
25	86	100.0	84	4	R21230 Human parathyroid hor	6.03e-02
26	86	100.0	84	4	R21231 Human parathyroid hor	6.03e-02
27	86	100.0	84	4	R21231 Human parathyroid hor	6.03e-02
28	86	100.0	84	4	R21212 Human parathyroid hor	6.03e-02
29	86	100.0	84	4	R23395 Porcine parathyroid ho	6.03e-02
30	86	100.0	84	4	R23283 Bovine parathyroid ho	6.03e-02
31	86	100.0	84	4	R21188 Human parathyroid hor	6.03e-02
32	86	100.0	84	4	R21189 Human parathyroid hor	6.03e-02
33	86	100.0	84	4	R21165 Human parathyroid hor	6.03e-02
34	86	100.0	84	4	R21164 Human parathyroid hor	6.03e-02
35	86	100.0	84	4	R23258 Bovine parathyroid ho	6.03e-02
36	86	100.0	84	4	R21168 Human parathyroid hor	6.03e-02
37	86	100.0	84	4	R23290 Bovine parathyroid ho	6.03e-02
38	86	100.0	84	4	R23402 Porcine parathyroid h	6.03e-02
39	86	100.0	84	4	R23275 Bovine parathyroid ho	6.03e-02
40	86	100.0	84	4	R23394 Porcine parathyroid h	6.03e-02
41	86	100.0	84	4	R21208 Human parathyroid hor	6.03e-02
42	86	100.0	84	4	R23904 Bovine parathyroid hor	6.03e-02
43	86	100.0	84	8	R42067 Human parathyroid hor	6.03e-02
44	86	100.0	84	8	R42067 Human parathyroid hor	6.03e-02
45	86	100.0	84	4	R23449 Porcine parathyroid h	6.03e-02

ALIGNMENTS

RESULT 1
ID R58024 standard; peptide; 38 AA.
AC R58024;
DT 20-SEP-1994 (first entry)
DE [Ala1, Ile2]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN G8269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (BAUO) SANDOZ LTD.
PA (BAUO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-PATENT GMBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage F, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 10; Page 35; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA.
Query Match 100.0%; Score 86; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.03e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 26 kklqdvhnfval 37

QY 1 KKLQDVHNFVAL 12

RESULT

2

ID P30015 standard; peptide: 44 AA.

AC P30015;

DT 11-SEP-1992 (first entry)

DE Human parathyroid hormone (1-44).

KW HPH; condensation; azide; active ester; carbodilimide.

OS Synthetic.

PN J57192350-A.

PD 26-NOV-1982.

PE 22-APR-1981; JP-059750.

PR 22-APR-1981; JP-059750.

PA (AJTN) TANPAKUSHITSU KENKY.

DR WPI; 83-03106K/02 (03106K).

PT Peptide fragment (1-44) of human parathyroid hormone - prepd. by

removing protecting gps. from condensed peptide

Claim 1, Page 1; 17pp; Japanese.

The peptide fragment (1-44) can be prepd. by condensn. of individual

amino acids or peptide fragments and removal of protecting groups

from the condensed peptide in conventional manner. The peptide bond

formation can be carried out pref. by azide method, active ester

method or carbodilimide method. No use is given.

Sequence 44 AA;

Query Match

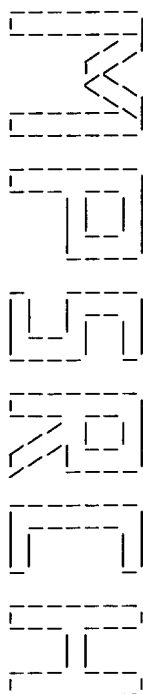
Best Local Similarity 100.0%; Score 86; DB 26; Length 44;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 kklqdvhnfval 37

QY 1 KKLQDVHNFVAL 12

Search completed: Thu Jul 30 10:44:56 1998
Job time : 22 secs.



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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:43:49 1998; Maspar time 3.30 Seconds
Tabular output not generated. 132.749 Million cell updates/sec

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A.pep
Perfect Score: 86
Sequence: 1 KKLQDVHNFVAL 12

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56

1:plr1 2:plr2 3:plr3 4:plr4 5:nr13d

Statistics: Mean 25.131; Variance 37.196; scale 0.676

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	86	100.0	34	5	12WE	parathyroid hormone (7.55e-06
2	86	100.0	34	5	12WE	parathyroid hormone (7.55e-06
3	86	100.0	34	5	12WE	parathyroid hormone (7.55e-06
4	86	100.0	35	5	12WD	parathyroid hormone (7.55e-06
5	86	100.0	36	5	12WB	parathyroid hormone (7.55e-06
6	86	100.0	37	5	12WB	parathyroid hormone (7.55e-06
7	86	100.0	37	5	12WB	parathyroid hormone (7.55e-06
8	86	100.0	37	5	12WB	parathyroid hormone (7.55e-06
9	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
10	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
11	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
12	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
13	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
14	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
15	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
16	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
17	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
18	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
19	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
20	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
21	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
22	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06
23	86	100.0	115	1	PTHD	parathyroid hormone (7.55e-06

24	54	62.8	1323	2	PN0568	connectin 3B - chicken	1.37e+01
25 <td>54</td> <td>62.8<td>3344<td>2<td>UQ1899<td>genome polypeptide -<th>1.37e+01</th></td></td></td></td></td>	54	62.8 <td>3344<td>2<td>UQ1899<td>genome polypeptide -<th>1.37e+01</th></td></td></td></td>	3344 <td>2<td>UQ1899<td>genome polypeptide -<th>1.37e+01</th></td></td></td>	2 <td>UQ1899<td>genome polypeptide -<th>1.37e+01</th></td></td>	UQ1899 <td>genome polypeptide -<th>1.37e+01</th></td>	genome polypeptide - <th>1.37e+01</th>	1.37e+01
26 <td>53</td> <td>61.6<td>49<td>2<td>S70651<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>49<td>2<td>S70651<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td>	49 <td>2<td>S70651<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td>	2 <td>S70651<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td>	S70651 <td>leukotriene-A4 hydrol<th>2.03e+01</th></td>	leukotriene-A4 hydrol <th>2.03e+01</th>	2.03e+01
27 <td>53</td> <td>61.6<td>145<td>5<td>1AT0<td>17-hedgenog 17-kda fr<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>145<td>5<td>1AT0<td>17-hedgenog 17-kda fr<th>2.03e+01</th></td></td></td></td>	145 <td>5<td>1AT0<td>17-hedgenog 17-kda fr<th>2.03e+01</th></td></td></td>	5 <td>1AT0<td>17-hedgenog 17-kda fr<th>2.03e+01</th></td></td>	1AT0 <td>17-hedgenog 17-kda fr<th>2.03e+01</th></td>	17-hedgenog 17-kda fr <th>2.03e+01</th>	2.03e+01
28 <td>53</td> <td>61.6<td>471<td>2<td>A46400<td>segment polarity prot<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>471<td>2<td>A46400<td>segment polarity prot<th>2.03e+01</th></td></td></td></td>	471 <td>2<td>A46400<td>segment polarity prot<th>2.03e+01</th></td></td></td>	2 <td>A46400<td>segment polarity prot<th>2.03e+01</th></td></td>	A46400 <td>segment polarity prot<th>2.03e+01</th></td>	segment polarity prot <th>2.03e+01</th>	2.03e+01
29 <td>53</td> <td>61.6<td>471<td>3<td>A43480<td>segmentation gene hed<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>471<td>3<td>A43480<td>segmentation gene hed<th>2.03e+01</th></td></td></td></td>	471 <td>3<td>A43480<td>segmentation gene hed<th>2.03e+01</th></td></td></td>	3 <td>A43480<td>segmentation gene hed<th>2.03e+01</th></td></td>	A43480 <td>segmentation gene hed<th>2.03e+01</th></td>	segmentation gene hed <th>2.03e+01</th>	2.03e+01
30 <td>53</td> <td>61.6<td>610<td>2<td>S20444<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>610<td>2<td>S20444<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td>	610 <td>2<td>S20444<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td>	2 <td>S20444<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td>	S20444 <td>leukotriene-A4 hydrol<th>2.03e+01</th></td>	leukotriene-A4 hydrol <th>2.03e+01</th>	2.03e+01
31 <td>53</td> <td>61.6<td>611<td>2<td>UN0066<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>611<td>2<td>UN0066<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td>	611 <td>2<td>UN0066<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td>	2 <td>UN0066<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td>	UN0066 <td>leukotriene-A4 hydrol<th>2.03e+01</th></td>	leukotriene-A4 hydrol <th>2.03e+01</th>	2.03e+01
32 <td>53</td> <td>61.6<td>611<td>2<td>S65947<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>611<td>2<td>S65947<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td></td>	611 <td>2<td>S65947<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td></td>	2 <td>S65947<td>leukotriene-A4 hydrol<th>2.03e+01</th></td></td>	S65947 <td>leukotriene-A4 hydrol<th>2.03e+01</th></td>	leukotriene-A4 hydrol <th>2.03e+01</th>	2.03e+01
33 <td>53</td> <td>61.6<td>632<td>2<td>S73824<td>MG242 homolog H91.orf<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>632<td>2<td>S73824<td>MG242 homolog H91.orf<th>2.03e+01</th></td></td></td></td>	632 <td>2<td>S73824<td>MG242 homolog H91.orf<th>2.03e+01</th></td></td></td>	2 <td>S73824<td>MG242 homolog H91.orf<th>2.03e+01</th></td></td>	S73824 <td>MG242 homolog H91.orf<th>2.03e+01</th></td>	MG242 homolog H91.orf <th>2.03e+01</th>	2.03e+01
34 <td>53</td> <td>61.6<td>1321<td>2<td>S27337<td>multidrug resistance<th>2.03e+01</th></td></td></td></td></td>	53	61.6 <td>1321<td>2<td>S27337<td>multidrug resistance<th>2.03e+01</th></td></td></td></td>	1321 <td>2<td>S27337<td>multidrug resistance<th>2.03e+01</th></td></td></td>	2 <td>S27337<td>multidrug resistance<th>2.03e+01</th></td></td>	S27337 <td>multidrug resistance<th>2.03e+01</th></td>	multidrug resistance <th>2.03e+01</th>	2.03e+01
35 <td>52</td> <td>60.5<td>314<td>2<td>S66274<td>annexin - pepper<th>2.98e+01</th></td></td></td></td></td>	52	60.5 <td>314<td>2<td>S66274<td>annexin - pepper<th>2.98e+01</th></td></td></td></td>	314 <td>2<td>S66274<td>annexin - pepper<th>2.98e+01</th></td></td></td>	2 <td>S66274<td>annexin - pepper<th>2.98e+01</th></td></td>	S66274 <td>annexin - pepper<th>2.98e+01</th></td>	annexin - pepper <th>2.98e+01</th>	2.98e+01
36 <td>52</td> <td>60.5<td>476<td>1<td>KCR152<td>stromelysin 2 (EC 3.4<th>2.98e+01</th></td></td></td></td></td>	52	60.5 <td>476<td>1<td>KCR152<td>stromelysin 2 (EC 3.4<th>2.98e+01</th></td></td></td></td>	476 <td>1<td>KCR152<td>stromelysin 2 (EC 3.4<th>2.98e+01</th></td></td></td>	1 <td>KCR152<td>stromelysin 2 (EC 3.4<th>2.98e+01</th></td></td>	KCR152 <td>stromelysin 2 (EC 3.4<th>2.98e+01</th></td>	stromelysin 2 (EC 3.4 <th>2.98e+01</th>	2.98e+01
37 <td>52</td> <td>60.5<td>606<td>2<td>S13526<td>hydrogenase homolog,<th>2.98e+01</th></td></td></td></td></td>	52	60.5 <td>606<td>2<td>S13526<td>hydrogenase homolog,<th>2.98e+01</th></td></td></td></td>	606 <td>2<td>S13526<td>hydrogenase homolog,<th>2.98e+01</th></td></td></td>	2 <td>S13526<td>hydrogenase homolog,<th>2.98e+01</th></td></td>	S13526 <td>hydrogenase homolog,<th>2.98e+01</th></td>	hydrogenase homolog, <th>2.98e+01</th>	2.98e+01
38 <td>52</td> <td>60.5<td>695<td>2<td>JC1493<td>follicle stimulating<th>2.98e+01</th></td></td></td></td></td>	52	60.5 <td>695<td>2<td>JC1493<td>follicle stimulating<th>2.98e+01</th></td></td></td></td>	695 <td>2<td>JC1493<td>follicle stimulating<th>2.98e+01</th></td></td></td>	2 <td>JC1493<td>follicle stimulating<th>2.98e+01</th></td></td>	JC1493 <td>follicle stimulating<th>2.98e+01</th></td>	follicle stimulating <th>2.98e+01</th>	2.98e+01
39 <td>52</td> <td>60.5<td>695<td>2<td>I45896<td>follicle stimulating<th>2.98e+01</th></td></td></td></td></td>	52	60.5 <td>695<td>2<td>I45896<td>follicle stimulating<th>2.98e+01</th></td></td></td></td>	695 <td>2<td>I45896<td>follicle stimulating<th>2.98e+01</th></td></td></td>	2 <td>I45896<td>follicle stimulating<th>2.98e+01</th></td></td>	I45896 <td>follicle stimulating<th>2.98e+01</th></td>	follicle stimulating <th>2.98e+01</th>	2.98e+01
40 <td>51</td> <td>59.3<td>201<td>2<td>C65188<td>hypothetical 22.3 kD<th>4.36e+01</th></td></td></td></td></td>	51	59.3 <td>201<td>2<td>C65188<td>hypothetical 22.3 kD<th>4.36e+01</th></td></td></td></td>	201 <td>2<td>C65188<td>hypothetical 22.3 kD<th>4.36e+01</th></td></td></td>	2 <td>C65188<td>hypothetical 22.3 kD<th>4.36e+01</th></td></td>	C65188 <td>hypothetical 22.3 kD<th>4.36e+01</th></td>	hypothetical 22.3 kD <th>4.36e+01</th>	4.36e+01
41 <td>51</td> <td>59.3<td>208<td>2<td>S20583<td>DNA-directed RNA poly<th>4.36e+01</th></td></td></td></td></td>	51	59.3 <td>208<td>2<td>S20583<td>DNA-directed RNA poly<th>4.36e+01</th></td></td></td></td>	208 <td>2<td>S20583<td>DNA-directed RNA poly<th>4.36e+01</th></td></td></td>	2 <td>S20583<td>DNA-directed RNA poly<th>4.36e+01</th></td></td>	S20583 <td>DNA-directed RNA poly<th>4.36e+01</th></td>	DNA-directed RNA poly <th>4.36e+01</th>	4.36e+01
42 <td>51</td> <td>59.3<td>232<td>2<td>S50292<td>ribosomal protein L16<th>4.36e+01</th></td></td></td></td></td>	51	59.3 <td>232<td>2<td>S50292<td>ribosomal protein L16<th>4.36e+01</th></td></td></td></td>	232 <td>2<td>S50292<td>ribosomal protein L16<th>4.36e+01</th></td></td></td>	2 <td>S50292<td>ribosomal protein L16<th>4.36e+01</th></td></td>	S50292 <td>ribosomal protein L16<th>4.36e+01</th></td>	ribosomal protein L16 <th>4.36e+01</th>	4.36e+01
43 <td>51</td> <td>59.3<td>476<td>1<td>KCHUS2<td>stromelysin 2 (EC 3.4<th>4.36e+01</th></td></td></td></td></td>	51	59.3 <td>476<td>1<td>KCHUS2<td>stromelysin 2 (EC 3.4<th>4.36e+01</th></td></td></td></td>	476 <td>1<td>KCHUS2<td>stromelysin 2 (EC 3.4<th>4.36e+01</th></td></td></td>	1 <td>KCHUS2<td>stromelysin 2 (EC 3.4<th>4.36e+01</th></td></td>	KCHUS2 <td>stromelysin 2 (EC 3.4<th>4.36e+01</th></td>	stromelysin 2 (EC 3.4 <th>4.36e+01</th>	4.36e+01
44 <td>51</td> <td>59.3<td>925<td>1<td>TVHUB8<td>transforming protein<th>4.36e+01</th></td></td></td></td></td>	51	59.3 <td>925<td>1<td>TVHUB8<td>transforming protein<th>4.36e+01</th></td></td></td></td>	925 <td>1<td>TVHUB8<td>transforming protein<th>4.36e+01</th></td></td></td>	1 <td>TVHUB8<td>transforming protein<th>4.36e+01</th></td></td>	TVHUB8 <td>transforming protein<th>4.36e+01</th></td>	transforming protein <th>4.36e+01</th>	4.36e+01
45 <td>51</td> <td>59.3<td>1444<td>1<td>AA3377<td>RNA-directed RNA poly<th>4.36e+01</th></td></td></td></td></td>	51	59.3 <td>1444<td>1<td>AA3377<td>RNA-directed RNA poly<th>4.36e+01</th></td></td></td></td>	1444 <td>1<td>AA3377<td>RNA-directed RNA poly<th>4.36e+01</th></td></td></td>	1 <td>AA3377<td>RNA-directed RNA poly<th>4.36e+01</th></td></td>	AA3377 <td>RNA-directed RNA poly<th>4.36e+01</th></td>	RNA-directed RNA poly <th>4.36e+01</th>	4.36e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		Structure	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung,	
COMMENT		pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT		Determination: NMR	
KEYWORDS		hormone	
FEATURE			
15-25			
SUMMARY		#region helix (right hand alpha)	
		length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 86; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 7.55e-06;	
Matches		12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	23	KKLQDVHNFVAL 34	
Qy	1	KKLQDVHNFVAL 12	
RESULT	2	12WG	#type complete
ENTRY		parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		TN003319	
#book		Marx, U.C.	
COMMENT		In Strukturen Verschiedener Parathormonfragmente in Loesung,	
		pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE 2-9
 15-25 #region helix (right hand alpha)\
 SUMMARY #region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 86; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.55e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 23 KKLQDVHNFVAL 34
 07 1 KKLQDVHNFVAL 12

Search completed: Thu Jul 30 10:44:16 1998
 Job time : 27 secs.

MIPS RELEASE

(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:42:38 1998; MasPar time 2.23 Seconds
134.872 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A.pep
Perfect Score: 86
Sequence: 1 KKLQDVHNFVAL 12

Scoring table:
PAM 150
Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 26.327; Variance 30.652; scale 0.859

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description	Pred. No.
1	86	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	5.76e-08
2	86	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	5.76e-08
3	86	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	5.76e-08
4	86	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	5.76e-08
5	84	97.7	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.95e-07
6	36	65.1	475	1	COG3_MOUSE STROMELYSIN-1 PRECURSOR	1.06e+00
7	36	65.1	475	1	COG3_RAT STROMELYSIN-1 PRECURSOR	1.06e+00
8	36	65.1	478	1	COG3_MOUSE STROMELYSIN-1 PRECURSOR	1.06e+00
9	36	65.1	651	1	TOP3_HAET DNA TOPOISOMERASE III	1.06e+00
10	55	64.0	693	1	FSHR_RAT FOLLICLE STIMULATING H	1.72e+00
11	55	64.0	693	1	FSHR_CHICK FOLLICLE STIMULATING H	1.72e+00
12	54	62.8	525	1	FSHR_HUMAN FOLLICLE STIMULATING H	1.72e+00
13	54	62.8	687	1	FSHR_HORSE FOLLICLE STIMULATING H	2.76e+00
14	54	62.8	694	1	FSHR_MOUSE FOLLICLE STIMULATING H	2.76e+00
15	54	62.8	3344	1	POLG_PRSVH GENOME POLYPROTEIN (CO	4.42e+00
16	53	61.6	471	1	HH_DROME HEMOGLOBIN PROTEIN PRECU	4.42e+00
17	53	61.6	609	1	LKHA_RAT LEUKOTRIENE A-4 HYDROL	4.42e+00
18	53	61.6	610	1	LKHA_HUMAN LEUKOTRIENE A-4 HYDROL	4.42e+00
19	53	61.6	610	1	LKHA_MOUSE LEUKOTRIENE A-4 HYDROL	4.42e+00
20	53	61.6	632	1	Y242_MYCPN HYPOTHELICAL PROTEIN M	4.42e+00
21	53	61.6	1321	1	MDRI_CAEEL MULTIDRUG RESISTANCE P	4.42e+00
22	52	60.5	476	1	COGX_RAT STROMELYSIN-2 PRECURSOR	7.01e+00
23	52	60.5	695	1	FSHR_BOVIN FOLLICLE STIMULATING H	7.01e+00

24	52	60.5	695	1	FSHR_SHEEP FOLLICLE STIMULATING H	7.01e+00
25	51	59.3	119	1	RT13_JACCA MITOCHONDRIAL RIBOSOMA	1.11e+01
26	51	59.3	200	1	YIGP_ECOLI HYPOTHELICAL 22.3 KD P	1.11e+01
27	51	59.3	232	1	RM16_YEAST PROBABLE MITOCHONDRIAL	1.11e+01
28	51	59.3	476	1	COGX_HUMAN STROMELYSIN-2 PRECURSOR	1.11e+01
29	51	59.3	636	1	RPOC_CYAPA DNA-DIRECTED RNA POLYM	1.11e+01
30	51	59.3	695	1	FSHR_PIG FOLLICLE STIMULATING H	1.11e+01
31	51	59.3	925	1	DBL_HUMAN PROTO-ONCOGENE DBL PRE	1.11e+01
32	51	59.3	1444	1	RRPL_RDV RNA-DIRECTED RNA POLYM	1.11e+01
33	50	58.1	203	1	RPOC_PROHO VEGEATIVE SPECIFIC PR	1.73e+01
34	50	58.1	316	1	VSH5_DICDI VEGEATIVE SPECIFIC PR	1.73e+01
35	50	58.1	462	1	COGM_MOUSE MACROPHAGE METALLOELAS	1.73e+01
36	50	58.1	470	1	COGM_HUMAN STROMELYSIN-1 PRECURSOR	1.73e+01
37	50	58.1	477	1	COG3_HUMAN STROMELYSIN-1 PRECURSOR	1.73e+01
38	50	58.1	543	1	VP61_NPVAC 61 KD PROTEIN	1.73e+01
39	50	58.1	831	1	TVID_SALTI VI POLYSACCHARIDE BIOS	1.73e+01
40	50	58.1	1177	1	MED_BACSV TRANSCRIPTION-REPAIR C	1.73e+01
41	50	58.1	1682	1	MSPL_PLAF3 MEMOZOITE SURFACE PROT	1.73e+01
42	50	58.1	1701	1	MSPL_PLAF3 MEMOZOITE SURFACE PROT	1.73e+01
43	50	58.1	1701	1	MSPL_PLAFW MEMOZOITE SURFACE PROT	1.73e+01
44	50	58.1	4349	1	DYHC_NECHA DYNEIN HEAVY CHAIN, CY	1.73e+01
45	49	57.0	908	1	ATMB_SALTY MG(2+) TRANSPORT ATPAS	2.69e+01

ALIGNMENTS

RESULT	ID	PTHY_CANFA	STANDARD;	PRT;	115 AA.
AC	P52212;				
DT	01-OCT-1996 (REL. 34, CREATED)				
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
OS	CANIS FAMILIARIS (DOG).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUETHERIA; CARNIVORA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PARATHYROID;				
RX	MEDLINE; 95369696.				
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,				
RL	GENE 160:241-243(1993).				
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN				
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.				
DR	EMBL: U15662; G558916; -				
DR	PROSITE; PS00335; PARATHYROID; 1.				
KW	HORMONE; SIGNAL.				
FT	SIGNAL.				
FT	PROPEP				
FT	CHAIN				
SQ	SEQUENCE				
Query Match					
Best Local Similarity	100.08;				
Matches	12; Conservative				
Db	57 KKLQDVHNFVAL 68				
Qy	1 KKLQDVHNFVAL 12				
RESULT	2				
ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.	
AC	P01268;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
OS	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				

Search completed: Thu Jul 30 10:42:44 1998
Job time : 6 secs.

```
OC EUTHERIA: ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAUDOUX J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T. JR., RICH A.;
RN PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037795.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RN PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RN GENE 28:319-329(1984).
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RL COHN D.V.;
RN PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAMSON B.F.,
RL AUBRACH G.D., POTTS J.T. JR.;
RN HOPPE-SEILER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREWER H.B. JR., ROMAN R.;
RN PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFLOS L.J., DAMSON B.F., HOGAN M.L., AUBRACH G.D.;
RN PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: J00106; G85; -
DR EMBL: J00023; G163641; -
DR EMBL: J00024; G163643; -
DR EMBL: J00024; E18248; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01938; G163647; -
DR EMBL: M25082; G163645; -
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
DR KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPER 26 31
FT CHAIN 32 115
FT CONFLICT 106 106 PARATHYROID HORMONE.
FT SEQUENCE 115 AA; 12980 MM; 673EASF2 CRC32;
V -> G (IN REF. 4).

Query Match 100.0%; Score 86; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. NO. 5,76e-08;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 57 KKLQDVHNHVAL 68
QY 1 KKLQDVHNHVAL 12
```

MIPS EMBL (TM)

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MSearch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:43:01 1998; Maspar time 3.89 Seconds
Tabular output not generated. 129,795 Million cell updates/sec

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A.pep
Perfect Score: 86
Sequence: 1 KKLQDVHNEVAL 12

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 25.060; Variance 31.683; scale 0.791

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	74	86.0	105	10	PARATHYROID HORMONE (F	2.00e-04
2	61	70.9	207	11	ORE36L	1.70e-01
3	60	69.8	342	11	SIMILAR TO BACTERIOPHA	2.77e-01
4	57	66.3	555	1	D8035.17P.	1.17e+00
5	56	65.1	477	4	MATRIX METALLOPROTEINA	1.87e+00
6	55	64.0	688	10	FOLICLE-STIMULATING H	2.97e+00
7	55	64.0	693	12	OVARIAN FOLLICLE-STIMU	2.97e+00
8	54	62.8	993	3	VINCULIN.	4.70e+00
9	54	62.8	1002	11	HC, P3 AND C1 PROTEINS	4.70e+00
10	54	62.8	1323	12	CONNECTIN (TITIN) (FRA	4.70e+00
11	54	62.8	3344	11	PRSV YK POLYPROTEIN.	4.70e+00
12	54	62.8	4162	12	CONNECTIN/TITIN (FRAGM	4.70e+00
13	53	61.6	299	3	SIMILAR TO SER/THR PRO	7.39e+00
14	53	61.6	1321	3	K08E7.9	7.39e+00
15	52	60.5	300	9	LYSR-TYPE BETA-LACTAMA	1.16e+01
16	52	60.5	314	8	ANNEXIN.	1.16e+01
17	52	60.5	345	9	STBA.	1.16e+01
18	52	60.5	606	9	HYD GAMMA.	1.16e+01
19	51	59.3	232	1	URAT CTP SYNTHETASE.	1.79e+01
20	51	59.3	591	3	F52E10.5 (FRAGMENT).	1.79e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	Q63473;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TTSSE-THYROID, AND PARATHYROID.			
RA	SCHMELZER H.J., GROSS G., MATER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -			
FT	NON_TER			
FT	SEQUENCE 1			
SO	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;			
DB	47	KLQDVHNEVAL 58		
OY	1	KLQDVHNEVAL 12		
RESULT	2	PRELIMINARY;	PRT;	207 AA.
ID	Q39628;			
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	ORE36L.			
OS	CYDIA POMONELLA GRANULOVIRUS.			
OC	VIRUSSES; DSDNA VIRUSES. NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	JEHLE J.A., VAN DER LINDEN I.F.A., VLAK J.M.;			
RL	VIRUS RES. 0:0-0(1997).			
DR	EMBL; AF002732; G2232189; -			
SO	SEQUENCE 207 AA; 23915 MW; D2F0E988 CRC32;			

Query Match 86.0%; Score 74; DB 10; Length 105;
Best Local Similarity 83.3%; Pred. No. 2.00e-04;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Thu Jul 30 13:38:03 1998

US-08-817-547A-20.rpt

Page 2

Query Match 70.9%; Score 61; DB 11; Length 207;
Best Local Similarity 66.7%; Pred. No. 1.70e-01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 144 RLOEVHDFV 152
:|:|:|:|
QY 2 KIQDVHNFV 10

Search completed: Thu Jul 30 10:43:30 1998
Job time : 29 secs.

NIH

(TW)

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MParch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:47:12 1998; MasPar time 2.77 Seconds
60.925 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-21
Description: (1-11) from US08817547A.pep
Perfect Score: 79
Sequence: 1 KLQDVHNEVAL 11

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 17.545; Variance 61.494; scale 0.285

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	79	100.0	37	2	R11882 Parathyroid hormone f	2.64e-01
2	79	100.0	38	9	R58024 [Ala1, Ile2]-hPTH(1-38	2.64e-01
3	79	100.0	38	9	R58022 [Ile1]-hPTH(1-38)-OH	2.64e-01
4	79	100.0	38	9	R58123 [Ser19]-hPTH(1-38)-OH	2.64e-01
5	79	100.0	38	9	R58124 [Lys19]-hPTH(1-38)-OH	2.64e-01
6	79	100.0	38	9	R58149 [Ile22]-hPTH(1-38)-OH	2.64e-01
7	79	100.0	38	9	R58152 [Arg22]-hPTH(1-38)-OH	2.64e-01
8	79	100.0	38	9	R58153 [Arg26]-hPTH(1-38)-OH	2.64e-01
9	79	100.0	38	9	R58120 [Ala17]-hPTH(1-38)-OH	2.64e-01
10	79	100.0	38	9	R58119 [Gly16]-hPTH(1-38)-OH	2.64e-01
11	79	100.0	44	26	P30015 Human parathyroid hor	2.64e-01
12	79	100.0	47	25	W21945 Human parathyroid hor	2.64e-01
13	79	100.0	84	27	W25687 Human parathyroid hor	2.64e-01
14	79	100.0	84	4	R23542 Bovine parathyroid h	2.64e-01
15	79	100.0	84	4	R23471 Porcine parathyroid h	2.64e-01
16	79	100.0	84	4	R23448 Porcine parathyroid h	2.64e-01
17	79	100.0	84	4	R23322 Bovine parathyroid ho	2.64e-01
18	79	100.0	84	4	R23345 Bovine parathyroid ho	2.64e-01
19	79	100.0	84	4	R23336 Bovine parathyroid ho	2.64e-01

20	79	100.0	84	4	R23429 Porcine parathyroid h	2.64e-01
21	79	100.0	84	4	R23259 Bovine parathyroid ho	2.64e-01
22	79	100.0	84	4	R23485 Porcine parathyroid h	2.64e-01
23	79	100.0	84	4	R21257 Human parathyroid hor	2.64e-01
24	79	100.0	84	4	R21156 Human parathyroid hor	2.64e-01
25	79	100.0	84	4	R23483 Porcine parathyroid h	2.64e-01
26	79	100.0	84	25	W29420 Human parathyroid hor	2.64e-01
27	79	100.0	84	4	R23549 Bovine parathyroid ho	2.64e-01
28	79	100.0	84	4	R23327 Bovine parathyroid hor	2.64e-01
29	79	100.0	84	4	R21213 Human parathyroid hor	2.64e-01
30	79	100.0	84	4	R21212 Human parathyroid hor	2.64e-01
31	79	100.0	84	4	R21238 Human parathyroid hor	2.64e-01
32	79	100.0	84	4	R21183 Human parathyroid hor	2.64e-01
33	79	100.0	84	4	R21188 Human parathyroid hor	2.64e-01
34	79	100.0	84	4	R21189 Human parathyroid hor	2.64e-01
35	79	100.0	84	4	R23258 Bovine parathyroid hor	2.64e-01
36	79	100.0	84	4	R21168 Human parathyroid hor	2.64e-01
37	79	100.0	84	4	R23425 Porcine parathyroid h	2.64e-01
38	79	100.0	84	4	R21241 Human parathyroid hor	2.64e-01
39	79	100.0	84	4	R21170 Human parathyroid hor	2.64e-01
40	79	100.0	84	4	R21169 Human parathyroid hor	2.64e-01
41	79	100.0	84	8	R42068 Stability-enhanced hu	2.64e-01
42	79	100.0	84	8	R42074 Stability-enhanced hu	2.64e-01
43	79	100.0	84	4	R23449 Porcine parathyroid h	2.64e-01
44	79	100.0	114	1	P80306 Sequence of bovine pa	2.64e-01
45	79	100.0	115	4	P40251 Protein sequence incl	2.64e-01

ALIGNMENTS

RESULT 1
ID R11882 standard; protein; 37 AA.
AC R11882;
DT 24-JUL-1991 (first entry)
DE Parathyroid hormone fragment (1-37).
KW Parathyroid hormone; osteoporosis; hypertension; hypoparathyroidism;
KW kidney failure; hypertension; acute renal insufficiency.
OS Homo sapiens.
PN DE3935738-A.
PD 08-MAY-1991.
PF 27-OCY-1989; 935738.
PR 27-OCY-1989; DE:935738.
PA (FORS.) FORSMANN W.
PI FORSMANN W-G, Herbst F, Schulz-Knappe P, Adermann K, Giegelmann M;
DR WPI; 91-141042/20.
PT New parathyroid hormone fragment and its naturally occurring
PT derivative. - used to treat osteoporosis, hypertension,
PT hypoparathyroidism, electrolyte imbalance associated with kidney
PT failure, etc.
PS Claim 1; page 6; 22pp; German.
CC This parathyroid hormone fragment, comprising residues 1-37, and its
CC derivs. are useful for treating parathyroid gland disorders,
CC degenerative bone disease, circulatory disease, lung disease, etc.
CC Antibodies raised against the fragment are useful for diagnosing
CC these diseases. The fragment and derivs. are administered as a
CC lyophilisate with mannitol.
SQ Sequence 37 AA:
Query Match 100.0%; Score 79; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.64e-01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 27 klqdvhnfval 37
QY 1 KLQDVHNEVAL 11
RESULT 2
ID R58024 standard; peptide; 38 AA.
AC R58024;
DT 20-SEP-1994 (first entry)
DE [Ala1, Ile2]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;

KM calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 OS Synthetic.
 PN GB2269176-A.
 PD 02-FEB-1994.
 PF 12-JUL-1993; 014384.
 PR 15-JUL-1992; GB-015009.
 PR 18-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 23-DEC-1992; GB-026861.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GRS MBH.
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
 Gombergt F, Gram H, Lewis I, Ramage P, Schneider H,
 Maechli R, Rainer A;
 WPI: 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 PS Example 10; Page 35; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 38 AA;

Query Match 100.0%; Score 79; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2,64e-01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 27 Klgdyhmfval 37
 |||||
 Oy 1 KLDVHNFVAL 11

Search completed: Thu Jul 30 10:47:36 1998
 Job time : 24 secs.

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(TM)

MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:46:26 1998; MasPar time 3.26 Seconds
Tabular output not generated. 123.145 Million cell updates/sec

Title: >US-08-817-547A-21
Description: (1-11) from US08817547A.pep
Perfect Score: 79
Sequence: 1 KLDVHNFVAL 11

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

plrs6
1:plrl 2:plrl 3:plrl 4:plrl 5:nrl3d

Statistics: Mean 24.418; Variance 35.126; scale 0.695

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	79	100.0	34	5 12WE	parathyroid hormone (7.53e-05	
2	79	100.0	34	5 12WG	parathyroid hormone (7.53e-05	
3	79	100.0	34	5 12WF	parathyroid hormone 4 7.53e-05	
4	79	100.0	35	5 12WD	parathyroid hormone (7.53e-05	
5	79	100.0	36	5 12WB	parathyroid hormone (7.53e-05	
6	79	100.0	37	5 12WH	parathyroid hormone (7.53e-05	
7	79	100.0	37	5 12WC	parathyroid hormone (7.53e-05	
8	79	100.0	115	1 PTHU	parathyroid hormone p 7.53e-05	
9	79	100.0	115	1 JCA202	parathyroid hormone p 7.53e-05	
10	79	100.0	115	1 PTHG	parathyroid hormone p 7.53e-05	
11	79	100.0	115	1 PTHB	parathyroid hormone p 7.53e-05	
12	77	97.5	115	1 A05091	parathyroid hormone p 2.03e-04	
13	67	84.8	105	5 151851	parathyroid hormone - 2.44e-02	
14	60	75.9	34	5 151851	cyclic parathyroid ho 5.75e-01	
15	60	75.9	34	5 151851	parathyroid hormone (5.75e-01	
16	53	67.1	555	2 S69641	hypothetical protein (1.11e+01	
17	53	67.1	632	2 S73824	M6242 homolog H91-ortf 1.11e+01	
18	53	67.1	1321	2 S27337	multidrug resistance 1.11e+01	
19	52	65.8	606	2 S13526	hydrogenase homolog, 2.48e+01	
20	51	64.6	201	2 C65188	hypothetical 22.3 kd 2.48e+01	
21	51	64.6	232	2 S50292	ribosomal protein l16 2.48e+01	
22	51	64.6	1444	1 A43377	RNA-directed RNA poly 2.48e+01	
23	50	63.3	217	2 E70126	hypothetical protein 3.67e+01	

24	50	63.3	462	2 A42401	macrophage elastase (3.67e+01
25	50	63.3	470	2 A49499	metalloelastase HME (3.67e+01
26	50	63.3	543	2 H40781	hypothetical 60.7k pr 3.67e+01
27	50	63.3	543	2 S25128	61k protein - Autogra 3.67e+01
28	50	63.3	653	2 S40449	pro-hormone convertas 3.67e+01
29	50	63.3	731	2 S28491	hypothetical protein 3.67e+01
30	50	63.3	831	2 D36892	V1PC 5'-region hypoch 3.67e+01
31	50	63.3	1323	2 PNU0568	connectin 3B - chickc 3.67e+01
32	49	62.0	142	2 B40535	clathrin-associated p 5.40e+01
33	49	62.0	145	5 1AT0	17-hedgehog 17-kda fr 5.40e+01
34	49	62.0	316	2 S07569	protein H5 - slime mo 5.40e+01
35	49	62.0	455	2 A26081	epoxide hydrolase (EC 5.40e+01
36	49	62.0	471	2 A46480	segment polarity prot 5.40e+01
37	49	62.0	471	2 A43480	segmentation gene hed 5.40e+01
38	49	62.0	475	1 KCRTH	stromelysin 1 (EC 3.4 5.40e+01
39	49	62.0	477	1 KCMSS1	stromelysin 1 (EC 3.4 5.40e+01
40	49	62.0	478	1 KCRBS1	stromelysin 1 (EC 3.4 5.40e+01
41	49	62.0	651	2 G64068	DNA topoisomerase (EC 5.40e+01
42	49	62.0	779	2 S50054	chloride channel prot 5.40e+01
43	49	62.0	1490	2 JC5145	DNA (cytosine-5'-)met 5.40e+01
44	49	62.0	1495	2 S22610	DNA (cytosine-5'-)met 5.40e+01
45	49	62.0	1537	2 JCA172	DNA (cytosine-5'-)met 5.40e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPRH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
COMMENT		In Strukturten Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Determination: NMR	
KEYWORDS		hormone	
FEATURE			
15-25			
SUMMARY		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 79; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 7.53e-05;	
Matches		11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	24	KLDVHNFVAL 34	
Qy	1	KLDVHNFVAL 11	
RESULT	2	12WG	#type complete
ENTRY		parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		TN003319	
#authors		Marx, U.C.	
COMMENT		In Strukturten Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 2-9
 15-25
 SUMMARY #region helix (right hand alpha)\
 #region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 79; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.53e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 KLDVHNFVAL 34
 |||||
 0y 1 KLDVHNFVAL 11

Search completed: Thu Jul 30 10:46:54 1998
 Job time : 28 secs.

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:45:13 1998; MasPar time 2.26 Seconds
122.035 Million cell updates/sec
Tabular output not generated.

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Title: >US-08-917-547A-21
Description: (1-11) from US08817547A.pep
Perfect Score: 79
Sequence: 1 KLDVHNFVAL 11

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residu

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

```

Statistics: Mean 25.575; Variance 28.974; scale 0.883

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Build No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	79	100.0	115	1	PTHX_CANFA	PARATHYROID HORMONE PR	1.01e-06
2	79	100.0	115	1	PTHX_BOVIN	PARATHYROID HORMONE PR	1.01e-06
3	79	100.0	115	1	PTHX_PIG	PARATHYROID HORMONE PR	1.01e-06
4	79	100.0	115	1	PTHX_HUMAN	PARATHYROID HORMONE PR	1.01e-06
5	77	97.5	115	1	PTHX_RAT	PARATHYROID HORMONE PR	3.45e-06
6	53	67.1	632	1	Y242_MJCNP	HYPOTHETICAL PROTEIN M	2.15e+00
7	53	67.1	1321	1	MDRI_CANEL	MULTIDRUG RESISTANCE P	2.15e+00
8	51	64.6	200	1	Y1GE_ECOLI	HYPOTHETICAL 22.3 KD P	5.64e+00
9	51	64.6	232	1	RM16_YEAST	PROBABLE MITOCHONDRIAL	5.64e+00
10	51	64.6	1444	1	RRPL_RRV	RNA-DIRECTED RNA POLYM	5.64e+00
11	50	63.3	462	1	COG6_MOUSE	MACROPHAGE METALLOELAS	9.04e+00
12	50	63.3	470	1	COG6_HUMAN	MACROPHAGE METALLOELAS	9.04e+00
13	50	63.3	543	1	VP61_NYVAC	61 KD PROTEIN.	9.04e+00
14	50	63.3	831	1	TVID_SALTI	VI POLYSACCHARIDE BIOS	9.04e+00
15	49	62.0	142	1	AP17_RAT	CIATHIRIN COAT ASSEMBLY	1.44e+01
16	49	62.0	142	1	AP17_HUMAN	CIATHIRIN COAT ASSEMBLY	1.44e+01
17	49	62.0	316	1	VSH5_DICDI	VEGETATIVE SPECIFIC PR	1.44e+01
18	49	62.0	455	1	HYEP_RAT	EPOXIDE HYDROLASE (EC	1.44e+01
19	49	62.0	471	1	HH_DROME	HEXHEHOG PROTEIN PRECU	1.44e+01
20	49	62.0	475	1	COG3_RAT	STROMELISIN-1 PRECURSO	1.44e+01
21	49	62.0	477	1	COG3_MOUSE	STROMELISIN-1 PRECURSO	1.44e+01
22	49	62.0	478	1	COG3_RABIT	STROMELISIN-1 PRECURSO	1.44e+01
23	49	62.0	651	1	TOP3_NAEIN	DNA TOPOISOMERASE III	1.44e+01

24	49	62.0	779	1	GEFI_YEAST	GEFI PROTEIN (VOLTAGE-	1.44e+01			
25	49	62.0	1495	1	MDDM_HUMAN	DNA (CYTOSINE-5)-METHY	1.44e+01			
26	48	60.8	136	1	V441_MYCN	HYPOTHETICAL PROTEIN M	2.27e+01			
27	48	60.8	153	1	M111_BRAE	MELANTONIN RECEPTOR TYP	2.27e+01			
28	48	60.8	317	1	Y600_HAETN	HYPOTHETICAL PROTEIN H	2.27e+01			
29	48	60.8	328	1	LDH_STRMG	L-LACTATE DEHYDROGENAS	2.27e+01			
30	48	60.8	398	1	YOFD_BACSU	HYPOTHETICAL 45.7 KD P	2.27e+01			
31	48	60.8	409	1	NADR_SALTY	TRANSCRIPTIONAL REGULA	2.27e+01			
32	48	60.8	410	1	NADR_ECOLI	TRANSCRIPTIONAL REGULA	2.27e+01			
33	48	60.8	692	1	FSHR_RAT	FOLLICLE STIMULATING H	2.27e+01			
34	48	60.8	693	1	FSHR_CHICK	FOLLICLE STIMULATING H	2.27e+01			
35	48	60.8	827	1	RED1_YEAST	RED1 PROTEIN.	2.27e+01			
36	48	60.8	881	1	HELI_YZVD	PROBABLE HELICASE.	2.27e+01			
37	48	60.8	933	1	CC54_YEAST	CELL DIVISION CONTROL	2.27e+01			
38	48	60.8	1318	1	V4VD_BPTI	INTERNAL VIRION PROTEI	2.27e+01			
39	48	60.8	1620	1	MDDM_MOUSE	DNA (CYTOSINE-5)-METHY	2.27e+01			
40	48	60.8	4725	1	DYHC_DICDI	DYNEIN HEAVY CHAIN, CY	2.27e+01			
41	47	59.5	274	1	COL_STYFL	T-CELL SURFACE GLYCOPR	3.55e+01			
42	47	59.5	649	1	PAFL_MOUSE	PAFL PROTEIN (PAS-ASSO	3.55e+01			
43	47	59.5	687	1	FSHR_EQUUS	FOLLICLE STIMULATING H	3.55e+01			
44	47	59.5	694	1	FSHR_HORSE	FOLLICLE STIMULATING H	3.55e+01			
45	47	59.5	3344	1	POLG_PRSVH	GENOME POLYPROTEIN (CO	3.55e+01			
ALIGNMENTS										
RESULT	1	STANDARD;	PRT;	115 AA.						
ID	PTRYX_CANFA									
AC	P521212;									
DT	01-OCT-1996 (REL. 34, CREATED)									
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)									
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)									
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).									
GN	PTH.									
OS	CANIS FAMILIARIS (DOG).									
OC	EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;									
CC	EUTHERIA; CANIYORA.									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	TISSUE-PARATHYROID;									
RX	MEDLINE; 95369696.									
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,									
RA	DEMILLÉ J.N., CAPEN C.C.;									
RL	GENE 160:241-243(1995).									
CC	-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN									
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.									
DR	EMBL; U15662; G558916; -.									
DR	PROSITE; PS00335; PARATHYROID; 1.									
KM	HORMONE; SIGNAL.									
FT	SIGNAL	1	25	BY SIMILARITY.						
FT	PROPEP	26	31	BY SIMILARITY.						
FT	CHAIN	32	115	PARATHYROID HORMONE.						
SO	SEQUENCE	115 AA;	12957 MM;	16ED0EBC	CRC32;					
Query Match										
Best Local Similarity		100.0%;	Score 79;	DB 1;	Length 115;					
Matches		11; Conservative	Pred. No. 1.0e-06;	0;	Mismatches 0;	Indels 0;	Gaps 0;			
DB	58	KL04DHFVAL 68								
OY	1	KL04DHFVAL 11								
RESULT 2										
ID	PTRYX_BOVIN	STANDARD;	PRT;	115 AA.						
AC	P01268;									
DT	21-JUL-1986 (REL. 01, CREATED)									
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)									
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)									
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).									
GN	PTH.									
OS	BOS TAURUS (BOVINE).									
OC	EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;									

Search completed: Thu Jul 30 10:45:20 1998
Job time : 7 secs.

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RA POTTS J.T. JR., RICH A.;
RA PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RA PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RA MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RA GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALI H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RA COHN D.V.;
RA PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALI H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RA AUBRACH G.D., POTTS J.T. JR.;
RA HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREWER H.B. JR., RONAN R.;
RA PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALI H.D., SAUER R.,
RA DEFOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.;
RA PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
RN [9]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
RN BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: V00106; 685; -
DR EMBL: J00023; G163641; -
DR EMBL: J00024; G163643; -
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01938; G163647; -
DR EMBL: M25082; G163645; -
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
KM HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 79; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.01e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 58 KLDVHNFVAL 68
OY 1 KLDVHNFVAL 11

WILEY
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:45:37 1998; MasPar time 3.84 Seconds
Tabular output not generated. 120.566 Million cell updates/sec

Title: >US-08-817-547A-21
Description: (1-11) from US08817547A.pep
Perfect Score: 79
Sequence: 1 KLDVHNFEVAL 11

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 24.328; Variance 30.213; scale 0.805
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	67	84.8	105	10	PARATHYROID HORMONE (F	3.43e-03
2	61	77.2	207	11	ORF36L.	7.88e-02
3	54	68.4	993	3	VINCULIN.	2.47e+00
4	53	67.1	342	11	SIMILAR TO BACTERIOPHA	3.95e+00
5	53	67.1	555	1	D8035.17P.	3.95e+00
6	53	67.1	1321	3	KOBE7.9.	3.95e+00
7	52	65.8	345	9	STBA.	6.28e+00
8	52	65.8	606	9	HYD GAMMA.	6.28e+00
9	51	64.6	232	1	URA7 CTP SYNTHETASE.	5.94e+00
10	51	64.6	1283	3	SIMILAR TO MULTIDRUG-R	9.94e+00
11	51	64.6	1444	11	RNA-DEPENDENT RNA POLY	9.94e+00
12	50	63.3	207	4	ARYLAUTAMINE N-ACETY	1.56e+01
13	50	63.3	360	9	HYDROGENASE SMALL SUBU	1.56e+01
14	50	63.3	402	12	FERROCHLATASE (EC 4.9	1.56e+01
15	50	63.3	463	10	MACROPHAGE METALLOLIS	1.56e+01
16	50	63.3	483	12	STROMELYSIN-1/2-A.	1.56e+01
17	50	63.3	653	3	PREPRO-HORMONE CONVERT	1.56e+01
18	50	63.3	653	3	NEUROENDOCRINE CONVERT	1.56e+01
19	50	63.3	660	3	PC2.	1.56e+01
20	50	63.3	761	3	SIMILAR TO THE ATP-BIN	1.56e+01

21	50	63.3	1254	3	SMR2.	1.56e+01
22	50	63.3	1323	12	CONNECTIN (TITIN) (FRA	1.56e+01
23	50	63.3	4162	12	CONNECTIN/TITIN (FRAG	1.56e+01
24	49	62.0	142	3	SIMILARITY TO CLATHRIN	2.44e+01
25	49	62.0	227	4	CYTCHROME P450 2C33V3	2.44e+01
26	49	62.0	227	4	CYTCHROME P450 2C33V1	2.44e+01
27	49	62.0	227	4	CYTCHROME P450 2C33V2	2.44e+01
28	49	62.0	299	3	SIMILAR TO SER/THR PRO	2.44e+01
29	49	62.0	455	10	MICROSOMAL EPOXIDE HYD	2.44e+01
30	49	62.0	477	4	MATRIX METALLOPROTEINA	2.44e+01
31	49	62.0	726	3	ATP-BINDING CASSETTE P	2.44e+01
32	49	62.0	732	3	MCMS HOMOLOG	2.44e+01
33	49	62.0	743	3	ZK250.1 PROTEIN.	2.44e+01
34	49	62.0	1190	3	F39B1.1 (FRAGMENT).	2.44e+01
35	49	62.0	1490	12	MODIFICATION METHYLASE	2.44e+01
36	49	62.0	1537	12	MODIFICATION METHYLASE	2.44e+01
37	49	62.0	1564	4	EPITHELIAL BASOLATELAR	2.44e+01
38	49	62.0	1774	3	EPITHELIAL BASOLATELAR	2.44e+01
39	49	62.0	1918	3	F2966.3B.	2.44e+01
40	49	62.0	1918	3	F2966.3A.	2.44e+01
41	48	60.8	232	9	DNA FOR DTD-P-RHANOSE	3.78e+01
42	48	60.8	377	3	T27A1.2 PROTEIN.	3.78e+01
43	48	60.8	453	1	HYPOTHETICAL 50.0 KD P	3.78e+01
44	48	60.8	693	12	OVARIAN FOLLICLE-STIMU	3.78e+01
45	48	60.8	787	9	PYRVATE FORMATE-LYASE	3.78e+01
			1289	3	SIMILARITY TO THE ATP-	3.78e+01

ALIGNMENTS

RESULT 1	PRELIMINARY: PRT: 105 AA.
ID 063473;	
AC 063473;	
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE PARATHYROID HORMONE (FRAGMENT).	
GN PTH.	
OS RATTUS NORVEGICUS (RAT).	
OC EUMAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
CC EUHARLIA; RODENTIA.	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE-THYROID, AND PARATHYROID;	
RA SCHMELZER H.J., GROSS G., MAYER H.;	
RL ADV. GENE TECHNOL. 21:228-229(1984).	
DR EMBL: M54875; G601933; -.	
FT NON-TER	
SEQ SEQUENCE 105 AA; 11746 MM; 6AC3163E CRC32;	
Query Match	84.8%; Score 67; DB 10; Length 105;
Best Local Similarity	81.8%; Pred. No. 3.43e-03;
Matches	9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 48 KLDGHNFEVAL 58	
QY 1 KLDVHNFEVAL 11	
RESULT 2	
ID 039628;	
AC 039628;	
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)	
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE ORF36L.	
OS CYTOA POMONELLA GRANULOVIRUS.	
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS.	
RN [1]	
RP SEQUENCE FROM N.A.	
RA JEHLE J.A., VAN DER LINDEN I.F.A., VLAK J.M.;	
RL VIRUS RES. 0:0-0(1997).	
DR EMBL: AF002732; G2232189; -.	
SEQ SEQUENCE 207 AA; 23915 MM; D2F0E988 CRC32;	

Query Match 77.2%; Score 61; DB 11; Length 207;
Best Local Similarity 66.7%; Pred. No. 7.88e-02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 144 RLOEVHDFV 152

QY 1 KLDVHNEV 9

Search completed: Thu Jul 30 10:46:08 1998
Job time : 31 secs.

W O S E I H (TM)

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Masrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:50:05 1998; MasPar time 2.64 Seconds
Tabular output not generated. 58.155 Million cell updates/sec

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A-pep
Perfect Score: 72
Sequence: 1 LGDVHNFVAL 10

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.979; Variance 58.346; scale 0.291
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	72	100.0	38	9	R58151 [Ser22]-hPTH(1-38)-OH	8.81e-01
2	72	100.0	38	9	R58153 [Arg26]-hPTH(1-38)-OH	8.81e-01
3	72	100.0	38	9	R58022 [Ile1]-hPTH(1-38)-OH	8.81e-01
4	72	100.0	38	9	R58140 [Phe21]-hPTH(1-38)-OH	8.81e-01
5	72	100.0	38	9	R58142 [Asn21]-hPTH(1-38)-OH	8.81e-01
6	72	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	8.81e-01
7	72	100.0	38	9	R58133 [Asp19]-hPTH(1-38)-OH	8.81e-01
8	72	100.0	44	26	P30015 Human parathyroid hor	8.81e-01
9	72	100.0	47	25	W25946 Fuslon protein compri	8.81e-01
10	72	100.0	84	27	W25687 Human parathyroid hor	8.81e-01
11	72	100.0	84	4	R23237 Human parathyroid hor	8.81e-01
12	72	100.0	84	4	R23192 Human parathyroid hor	8.81e-01
13	72	100.0	84	4	R23309 Bovine parathyroid ho	8.81e-01
14	72	100.0	84	4	R23276 Bovine parathyroid ho	8.81e-01
15	72	100.0	84	4	R23254 Human parathyroid hor	8.81e-01
16	72	100.0	84	4	R23429 Porcine parathyroid h	8.81e-01
17	72	100.0	84	4	R23259 Bovine parathyroid ho	8.81e-01
18	72	100.0	84	4	R23485 Porcine parathyroid h	8.81e-01
19	72	100.0	84	4	R21257 Human parathyroid hor	8.81e-01

20	72	100.0	84	4	R23424 Porcine parathyroid h	8.81e-01
21	72	100.0	84	4	R23383 Porcine parathyroid h	8.81e-01
22	72	100.0	84	5	R29568 Oxidation resistant l	8.81e-01
23	72	100.0	84	5	R29563 Oxidation resistant p	8.81e-01
24	72	100.0	84	4	R23483 Porcine parathyroid h	8.81e-01
25	72	100.0	84	25	W29420 Human parathyroid hor	8.81e-01
26	72	100.0	84	5	R29562 Oxidation resistant l	8.81e-01
27	72	100.0	84	5	R29561 Oxidation resistant p	8.81e-01
28	72	100.0	84	4	R23339 Bovine parathyroid h	8.81e-01
29	72	100.0	84	4	R23272 Bovine parathyroid ho	8.81e-01
30	72	100.0	84	4	R23301 Bovine parathyroid ho	8.81e-01
31	72	100.0	84	4	R23294 Bovine parathyroid ho	8.81e-01
32	72	100.0	84	4	R23242 Human parathyroid hor	8.81e-01
33	72	100.0	84	4	R21229 Human parathyroid hor	8.81e-01
34	72	100.0	84	4	R21181 Human parathyroid hor	8.81e-01
35	72	100.0	84	4	R23227 Human parathyroid hor	8.81e-01
36	72	100.0	84	4	R23507 Porcine parathyroid h	8.81e-01
37	72	100.0	84	4	R23264 Bovine parathyroid ho	8.81e-01
38	72	100.0	84	4	R23248 Bovine parathyroid hor	8.81e-01
39	72	100.0	84	4	R21250 Human parathyroid hor	8.81e-01
40	72	100.0	84	4	R23456 Porcine parathyroid h	8.81e-01
41	72	100.0	84	4	R23363 Bovine parathyroid ho	8.81e-01
42	72	100.0	84	4	R21180 Human parathyroid hor	8.81e-01
43	72	100.0	84	4	R23423 Porcine parathyroid h	8.81e-01
44	72	100.0	84	4	R23449 Porcine parathyroid h	8.81e-01
45	72	100.0	115	4	P40251 Protein sequence incl	8.81e-01

ALIGNMENTS

RESULT 1
ID R58151 standard; peptide; 38 AA.

AC R58151;
DT 20-SEP-1994 (first entry)
DE [Ser22]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW Calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PF 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.

PA (SANO) SANDOZ LTD.
PA (BAUE) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
PI Waelchli R, Rainer A;
DR WPI, 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

PS Example 148; Page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 72; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.81e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Db 28 lgdvhmfval 37

OY 1 LQDVHNFVAL 10

RESULT 2
ID RS8153 standard; peptide; 38 AA.
AC RS8153;
DE 20-SEP-1994 (first entry)
DE [Arg26]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB226917C-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001691.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUER) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI; 94-018352/03
PT New active para-thyroid hormone variants - used for treating or
PT Preventing osteoporosis etc.
PS Example 150: Page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 72; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.81e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB 28 lqdvhnfv al 37
1 LQDVHNFVAL 10

Search completed: Thu Jul 30 10:50:20 1998
Job time : 15 secs.

MISRESEARCH
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:49:12 1998; Maspar time 3.29 Seconds
111.059 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A.pep
Perfect Score: 72
Sequence: 1 LODVHNFEVAL 10

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 4% summaries

Database: p156
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 23.774; Variance 33.625; scale 0.707

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	72	100.0	34	5 12WE	parathyroid hormone (1.05e-03	
2	72	100.0	34	5 12WE	parathyroid hormone (1.05e-03	
3	72	100.0	34	5 12WE	parathyroid hormone (1.05e-03	
4	72	100.0	35	5 12WD	parathyroid hormone (1.05e-03	
5	72	100.0	36	5 12WB	parathyroid hormone (1.05e-03	
6	72	100.0	37	5 12WB	parathyroid hormone (1.05e-03	
7	72	100.0	37	5 12WB	parathyroid hormone (1.05e-03	
8	72	100.0	115	2 JCA202	parathyroid hormone p 1.05e-03	
9	72	100.0	115	2 JCA202	parathyroid hormone p 1.05e-03	
10	72	100.0	115	1 P78G	parathyroid hormone p 1.05e-03	
11	72	100.0	115	1 P78G	parathyroid hormone p 1.05e-03	
12	70	97.2	115	2 A05091	parathyroid hormone p 2.81e-03	
13	60	83.3	105	2 I51851	parathyroid hormone p 3.11e-01	
14	53	73.6	34	5 12WA	parathyroid hormone (6.64e+00	
15	53	73.6	34	5 12WA	parathyroid hormone (6.64e+00	
16	53	73.6	632	2 S73824	MG242 homolog H91-ort 6.64e+00	
17	52	72.2	606	2 S13526	hydrogenase homolog, 1.01e+01	
18	51	70.8	201	2 C65188	hypothetical 22.3 kd 1.35e+01	
19	50	69.4	217	2 E70126	hypothetical protein 2.29e+01	
20	50	69.4	543	2 H40781	hypothetical 60.7K pr 2.29e+01	
21	50	69.4	543	2 S25128	61k protein - Autogra 2.29e+01	
22	50	69.4	653	2 S40449	pro-hormone convertas 2.29e+01	
23	50	69.4	731	2 S28491	hypothetical protein 2.29e+01	

24	50	69.4	831	2 D36892	V1PC 5'-region hypoth	2.29e+01
25	49	68.1	142	2 B40535	clathrin-associated p	3.43e+01
26	49	68.1	316	2 S07569	protein H5 - slime mo	3.43e+01
27	49	68.1	455	2 A26081	epoxide hydrolase (EC	3.43e+01
28	49	68.1	1321	2 S27337	multidrug resistance	3.43e+01
29	49	68.1	1490	2 JC5145	DNA (cytosine-5')-met	3.43e+01
30	49	68.1	1495	2 S22610	DNA (cytosine-5')-met	3.43e+01
31	49	68.1	1537	2 UC4172	DNA (cytosine-5')-met	3.43e+01
32	48	66.7	136	2 S73520	MG441 homolog E09-ort	5.09e+01
33	48	66.7	145	5 1AT0	hypothetical protein	5.09e+01
34	48	66.7	326	2 S76954	17-hedgehog 17-kda fr	5.09e+01
35	48	66.7	328	2 A43598	L-lactate dehydrogena	5.09e+01
36	48	66.7	398	2 D69952	conserved hypothetical	5.09e+01
37	48	66.7	452	2 S77436	sigma factor s16g reg	5.09e+01
38	48	66.7	471	3 A43480	segmentation gene hed	5.09e+01
39	48	66.7	471	2 A46400	segment polarity prot	5.09e+01
40	48	66.7	653	2 S27270	prohormone convertase	5.09e+01
41	48	66.7	881	1 W2BE55	gene 55 protein - hum	5.09e+01
42	48	66.7	1318	1 H1BPD7	internal vitron prote	5.09e+01
43	48	66.7	1612	2 UC5210	DNA (cytosine-5')-met	5.09e+01
44	47	65.3	240	2 F4676	biotin synthesis prot	7.52e+01
45	47	65.3	494	2 S13101	cytochrome P450 c117	7.52e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		Structure of human parathyroid hormone fragment 4-37, NMR 10	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		IN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	
KEYWORDS		Determination: NMR	
FEATURE		hormone	
SUMMARY		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 72; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.05e-03;	
Matches		10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	25	LODVHNFEVAL 34	
Qy	1	LODVHNFEVAL 10	
RESULT	2	12WG	#type complete
ENTRY		parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		IN003319	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	

```

COMMENT      Determination: NMR
KEYWORDS     disease mutation; hormone; signal
FEATURE      2-9      #region helix (right hand alpha)\
15-25        #region helix (right hand alpha)
SUMMARY      #length 34 #molecular-weight 4128 #checksum 5508

Query Match      100.0%; Score 72; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.05e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      25 LQDVHNFVAL 34
      |||||
QY      1 LQDVHNFVAL 10

Search completed: Thu Jul 30 10:49:46 1998
Job time : 34 secs.

```

N O T E S

(TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:47:53 1998; Maspar time 2.15 Seconds
Tabular output not generated. 116.508 Million cell updates/sec

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A.pep
Perfect Score: 72
Sequence: 1 LODVHNFVAL 10

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swissl1

Statistics: Mean 24.901; Variance 27.707; scale 0.899

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match	Length	ID	Description	Pred. No.
1	72	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	2.56e-05
2	72	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	2.56e-05
3	72	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	2.56e-05
4	72	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	2.56e-05
5	70	97.2	115	1	PTHY_RAT PARATHYROID HORMONE PR	8.57e-05
6	53	73.6	632	1	Y242_MYCPN HYPOTHETICAL PROTEIN M	1.14e+00
7	51	70.8	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	3.11e+00
8	50	69.4	543	1	VP61_NPVAC 61 KD PROTEIN.	5.08e+00
9	49	68.1	831	1	EVID_SALTI VI POLYSACCHARIDE BIOS	8.24e+00
10	49	68.1	142	1	AP17_HUMAN CLATHRIN COAT ASSEMBLY	8.24e+00
11	49	68.1	142	1	AP17_RAT CLATHRIN COAT ASSEMBLY	8.24e+00
12	49	68.1	316	1	VSH5_DICDI VEGETATIVE SPECIFIC PR	8.24e+00
13	49	68.1	455	1	HYEP_RAT EPOXIDE HYDROLASE (EC	8.24e+00
14	49	68.1	1321	1	MDR1_CAEL MULTIDRUG RESISTANCE P	8.24e+00
15	49	68.1	1495	1	MTDM_HUMAN DNA (CYTOSINE-5)-METHY	8.24e+00
16	48	66.7	136	1	V441_MYCPN HYPOTHETICAL PROTEIN M	1.32e+01
17	48	66.7	153	1	MIL1_BRARE MELANOTIN RECEPTOR TYP	1.32e+01
18	48	66.7	328	1	LDR_STRMU L-LACTATE DEHYDROGENAS	1.32e+01
19	48	66.7	398	1	YQPD_BACSU HYPOTHETICAL 45.7 KD P	1.32e+01
20	48	66.7	471	1	HH_DROME HEDGEHOG PROTEIN PRECU	1.32e+01
21	48	66.7	881	1	HELI_VZVD PROBABLE HELICASE.	1.32e+01
22	48	66.7	1318	1	VIVD_BPT7 INTERNAL VIRION PROTEI	1.32e+01
23	48	66.7	1620	1	MTDM_MOUSE DNA (CYTOSINE-5)-METHY	1.32e+01

24	47	65.3	125	1	Y4WJ_RHISN HYPOTHETICAL 13.3 KD P	2.11e+01
25	47	65.3	251	1	AGAI_ECOLI PUTATIVE GALACTOSAMINE	2.11e+01
26	47	65.3	274	1	CD1_STYFL T-CELL SURFACE GLYCOPR	2.11e+01
27	47	65.3	494	1	CPGN_RAT CYTOCHROME P450 IIC23	2.11e+01
28	47	65.3	589	1	KY28_MYCTU PROBABLE SERINE/THRON	2.11e+01
29	47	65.3	700	1	ADBL_YEAST PROBABLE BETA-ADAPTIN	2.11e+01
30	47	65.3	925	1	DBL_HUMAN PROTO-ONCOGENE DBL PRE	2.11e+01
31	47	65.3	1444	1	RRLV_RDV RNA-DIRECTED RNA POLYM	3.34e+01
32	46	63.9	435	1	PERC_LACLC AMINOPEPTIDASE C (EC 3	3.34e+01
33	46	63.9	469	1	NIFN_RHISN NITROGENASE IRON-MOLYB	3.34e+01
34	46	63.9	964	1	YBS9_YEAST HYPOTHETICAL 110.3 KD	3.34e+01
35	46	63.9	4344	1	DYHC_EMENT DYNENIN HEAVY CHAIN, CY	3.34e+01
36	45	62.5	104	1	YHY2_LACHE HYPOTHETICAL 11.8 KD P	5.24e+01
37	45	62.5	120	1	YGX0_YEAST HYPOTHETICAL 14.1 KD P	5.24e+01
38	45	62.5	297	1	YMY9_YEAST HYPOTHETICAL 34.0 KD P	5.24e+01
39	45	62.5	303	1	APPC_BACSU OLIGOPEPTIDE TRANSPORT	5.24e+01
40	45	62.5	490	1	CPGQ_MESAU CYTOCHROME P450 IIC26	5.24e+01
41	45	62.5	505	1	YXD2_CAEL PUTATIVE SERINE CARBOX	5.24e+01
42	45	62.5	687	1	CSTA_HELPY CARBON STARVATION PROT	5.24e+01
43	45	62.5	1247	1	YMF6_CAEL HYPOTHETICAL 139.9 KD	5.24e+01
44	45	62.5	2504	1	FAS_HUMAN FATTY ACID SYNTHASE (E	5.24e+01
45	45	62.5	2505	1	FAS_RAT FATTY ACID SYNTHASE (E	5.24e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	115 AA.
ID	PTHY_CANFA			
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EURAROTIA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; CARNIVORA.			
NC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PARATHYROID;			
RX	MEDLINE: 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RA	DEVILLE J.W., CAPEN C.C.;			
RL	GENE 160:241-243(1995).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
CC	EMBL: U15662; G558916; -			
DR	PROSITE; PS00335; PARATHYROID: 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL	1	25	BY SIMILARITY.
FT	PROPEP	26	31	BY SIMILARITY.
FT	CHAIN	32	115	PARATHYROID HORMONE.
SQ	SEQUENCE	115 AA; 12957 MW; 16DEDEBC CRC32;		
Query Match 100.0%; Score 72; DB 1; Length 115;				
Best Local Similarity 100.0%; Pred. No. 2.56e-05;				
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	59 LODVHNFVAL 68			
Qy	1 LODVHNFVAL 10			
RESULT 2 STANDARD; PRT; 115 AA.				
ID	PTHY_BOVIN			
AC	P01268;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	BOS TAURUS (BOVINE).			
OC	EURAROTIA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

Search completed: Thu Jul 30 10:47:59 1998
Job time : 6 secs.

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056517.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T. JR., RICH A.;
RN PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RP [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RP [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RP [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RN GENE 28:319-329(1984).
RP [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RL COHN D.V.;
RN PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RP [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RA AURBACH G.D., POTTS J.T. JR.;
RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RP [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREWER H.B. JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RP [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; J00106; G85; -;
DR EMBL; J00023; G163641; -;
DR EMBL; J00024; G163643; -;
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; K0138; E18250; ALT_INIT.
DR EMBL; M25082; G163647; -;
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;
V -> G (IN REF. 4).
PARATHYROID HORMONE.
Query Match 100.0%; Score 72; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.56e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 59 LODVNFVAL 68
QY 1 LODVNFVAL 10

W O S E H
(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:48:18 1998; Maspar time 3.79 Seconds
111.185 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A.pep
Perfect Score: 72
Sequence: 1 LODVHNFVAL 10

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 23.635; Variance 29.603; scale 0.798
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	60	83.3	105 10	063473	PARATHYROID HORMONE (F	8.41e-02
2	57	79.2	207 11	039628	ORE36L.	3.80e-01
3	54	75.0	993 3	017162	VINCULIN.	1.64e+00
4	52	72.2	345 9	P95793	STBA.	4.22e+00
5	52	72.2	606 9	046606	HYD GAMMA.	4.22e+00
6	50	69.4	653 3	016872	PREPRO-HORMONE CONVERT	1.06e+01
7	50	69.4	653 3	008845	NEUROENDOCRINE CONVERT	1.06e+01
8	50	69.4	660 3	016973	PC2.	1.06e+01
9	49	68.1	142 3	019123	SIMILARITY TO CLATHRIN	1.67e+01
10	49	68.1	207 4	029495	ARYALKYLAMINE N-ACETY	1.67e+01
11	49	68.1	227 4	028974	CYTOSOLIC P450 2C33V3	1.67e+01
12	49	68.1	227 4	028873	CYTOSOLIC P450 2C33V2	1.67e+01
13	49	68.1	227 4	028972	CYTOSOLIC P450 2C33V1	1.67e+01
14	49	68.1	229 3	019742	SIMILAR TO SER/THR PRO	1.67e+01
15	49	68.1	455 10	P97869	MICROSOMAL EPOXIDE HYD	1.67e+01
16	49	68.1	1190 3	020187	F39B1.1 (FRAGMENT).	1.67e+01
17	49	68.1	1321 3	021349	ROB87.9.	1.67e+01
18	49	68.1	1480 12	P79822	MODIFICATION METHYLASE	1.67e+01
19	49	68.1	1537 12	092072	MODIFICATION METHYLASE	1.67e+01
20	48	66.7	117 11	084562	GENOME, PARTIAL SEQUEN	2.61e+01

21	48	66.7	326 9	P74746	HYPOTHETICAL 36.0 KD P	2.61e+01
22	48	66.7	377 3	017273	T27A1.2 PROTEIN.	2.61e+01
23	48	66.7	440 9	055301	COTTA GENE (ORE440), CO	2.61e+01
24	48	66.7	452 9	P73256	SIGNA FACTOR SIBG REGU	2.61e+01
25	48	66.7	516 3	018198	SIMILAR TO K12H4.7 AND	2.61e+01
26	48	66.7	542 11	011448	VP78.	2.61e+01
27	48	66.7	653 3	025409	STAGNALIS LPC2.	2.61e+01
28	48	66.7	708 2	092542	MYELOBLAST KIAA0253 (F	2.61e+01
29	48	66.7	787 9	032797	PYRUVATE FORMATE-LYASE	2.61e+01
30	48	66.7	787 9	032799	PYRUVATE FORMATE-LYASE	2.61e+01
31	48	66.7	1149 3	023315	ZC434.5	2.61e+01
32	48	66.7	1612 3	027746	MODIFICATION METHYLASE	2.61e+01
33	47	65.3	207 4	002785	ARYALKYLAMINE-N-ACETY	4.04e+01
34	47	65.3	240 9	025846	BIOTIN SYNTHESIS PROTE	4.04e+01
35	47	65.3	485 1	005160	ALPHA-AGULTININ (AG-A	4.04e+01
36	47	65.3	494 10	064534	CYTOSOLIC P450 (EC 1.	4.04e+01
37	47	65.3	620 10	035488	VERY-LONG-CHAIN ACYL-C	4.04e+01
38	47	65.3	939 3	015799	STRAIN DD2 HEAT SHOCK	4.04e+01
39	47	65.3	939 3	015790	STRAIN 7G8 CG9 (CG9) A	4.04e+01
40	47	65.3	950 3	015788	STRAIN HB3 CG9 (CG9) A	4.04e+01
41	47	65.3	1444 11	098631	RNA-DEPENDENT RNA POLY	4.04e+01
42	46	63.9	402 12	042479	FERRICHELATASE (EC 4.9	6.22e+01
43	46	63.9	709 3	015783	HYBRID HISTIDINE KINAS	6.22e+01
44	46	63.9	1758 3	022830	SIMILAR TO HUMAN SREBP	6.22e+01
45	46	63.9	1825 10	P97394	ACTIN-CROSSLINKING PRO	6.22e+01

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	105 AA.
ID	063473;			
AC	063473;			
DT	01-NOV-1996 (TREMREL. 01, CREATED)			
DT	01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-THYROID; AND PARATHYROID;			
RA	SCHMELZER H.J., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -.			
FT	NON-TER			
SQ	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;			

Query Match 83.3%; Score 60; DB 10; Length 105;
Best Local Similarity 80.0%; Pred. No. 8.41e-02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB	49 LODGHNFVAL 58
QY	1 LODVHNFVAL 10
RESULT	2
ID	039628
AC	039628;
DT	01-JAN-1998 (TREMREL. 05, CREATED)
DT	01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
DT	01-JAN-1998 (TREMREL. 05, LAST ANNOTATION UPDATE)
DE	ORE36L.
OS	CYDIA POMONELLA GRANDULOVIRUS.
OC	VIRUSES; DSDNA VIRUSES; NO RNA STAGE; BACULOVIRIDAE; GRANDULOVIRUS.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	JEHL J.A., VAN DER LINDEN I.F.A., VLAK J.M.;
RL	VIRUS RES. 0:0-0(1997)
DR	EMBL; AF002732; G2232189; -.
SQ	SEQUENCE 207 AA; 23915 MW; D2F0E988 CRC32;

Query Match 79.2%; Score 57; DB 11; Length 207;
 Best Local Similarity 75.0%; Pred. No. 3.80e-01;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 145 LOEVHDFV 152
 ||:||:|
 QY 1 LODVHNFV 8

Search completed: Thu Jul 30 10:48:55 1998
 Job time : 37 secs.

WORLDWIDE
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:52:34 1998; MasPar time 2.61 Seconds
Tabular output not generated. 52.799 Million cell updates/sec

Title: >US-08-817-547A-23
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 QDVHNFVAL 9

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.221; Variance 50.458; scale 0.321

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	64	100.0	38	9	R58151	[Ser22]-hPTH(1-38)-OH	1.84e+00
2	64	100.0	38	9	R58142	[Asn21]-hPTH(1-38)-OH	1.84e+00
3	64	100.0	38	9	R58140	[Phe21]-hPTH(1-38)-OH	1.84e+00
4	64	100.0	38	9	R58129	[His19]-hPTH(1-38)-OH	1.84e+00
5	64	100.0	38	9	R58133	[Asp19]-hPTH(1-38)-OH	1.84e+00
6	64	100.0	44	26	P30015	Human parathyroid hor	1.84e+00
7	64	100.0	47	26	P21945	Fusion protein compri	1.84e+00
8	64	100.0	47	27	W25687	Human parathyroid hor	1.84e+00
9	64	100.0	84	4	R23337	Human parathyroid hor	1.84e+00
10	64	100.0	84	4	R21192	Human parathyroid hor	1.84e+00
11	64	100.0	84	4	R23309	Bovine parathyroid ho	1.84e+00
12	64	100.0	84	4	R21199	Human parathyroid hor	1.84e+00
13	64	100.0	84	4	R23376	Bovine parathyroid ho	1.84e+00
14	64	100.0	84	4	R21254	Human parathyroid hor	1.84e+00
15	64	100.0	84	4	R23429	Porcine parathyroid h	1.84e+00
16	64	100.0	84	4	R23259	Bovine parathyroid ho	1.84e+00
17	64	100.0	84	4	R23492	Porcine parathyroid h	1.84e+00
18	64	100.0	84	4	R23493	Porcine parathyroid h	1.84e+00
19	64	100.0	84	4	R23424	Porcine parathyroid h	1.84e+00

20	64	100.0	84	4	R23383	Porcine parathyroid h	1.84e+00
21	64	100.0	84	5	R29566	Oxidation resistant [1.84e+00
22	64	100.0	84	5	R29563	Oxidation resistant p	1.84e+00
23	64	100.0	84	4	R21240	Human parathyroid hor	1.84e+00
24	64	100.0	84	25	W29420	Human parathyroid hor	1.84e+00
25	64	100.0	84	5	R29562	Oxidation resistant [1.84e+00
26	64	100.0	84	5	R29561	Oxidation resistant p	1.84e+00
27	64	100.0	84	4	R21250	Human parathyroid hor	1.84e+00
28	64	100.0	84	4	R21181	Human parathyroid hor	1.84e+00
29	64	100.0	84	4	R23272	Bovine parathyroid hor	1.84e+00
30	64	100.0	84	4	R23242	Human parathyroid hor	1.84e+00
31	64	100.0	84	4	R23339	Bovine parathyroid hor	1.84e+00
32	64	100.0	84	4	R23248	Human parathyroid hor	1.84e+00
33	64	100.0	84	4	R23227	Human parathyroid hor	1.84e+00
34	64	100.0	84	4	R23232	Human parathyroid hor	1.84e+00
35	64	100.0	84	4	R21217	Human parathyroid hor	1.84e+00
36	64	100.0	84	4	R23279	Bovine parathyroid ho	1.84e+00
37	64	100.0	84	4	R23278	Bovine parathyroid ho	1.84e+00
38	64	100.0	84	4	R23433	Porcine parathyroid h	1.84e+00
39	64	100.0	84	4	R23456	Porcine parathyroid h	1.84e+00
40	64	100.0	84	4	R23363	Bovine parathyroid ho	1.84e+00
41	64	100.0	84	4	R21210	Human parathyroid hor	1.84e+00
42	64	100.0	84	4	R21211	Human parathyroid hor	1.84e+00
43	64	100.0	84	4	R23449	Porcine parathyroid h	1.84e+00
44	64	100.0	115	4	P40251	Porcine sequence incl	1.84e+00
45	64	100.0	229	9	R47971	Sequence of a full-le	1.84e+00

ALIGNMENTS

RESULT 1
ID R58151 standard; peptide: 38 AA.
AC R58151:
DT 20-SEP-1994 (first entry)
DE [Ser22]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PF 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) SANDOZ LTD.
PA (BAUE/) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERM GBS MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 148: Page 40: 92pp: English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA:

Query Match 100.0%; Score 64; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.84e+00;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 qdvhnfval 37

QY 1 QDVHNFVAL 9

RESULT 2
ID R58142 standard; peptide; 38 AA.
AC R58142;
DT 20-SEP-1994 (first entry)
DE [Asn21]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUER) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 139; Page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 64; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.84e+00;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 qdvhnfval 37
1 QDVHNFVAL 9

Search completed: Thu Jul 30 10:52:49 1998
Job time : 15 secs.


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COMMENT      Determination: NMR
KEYWORDS     disease mutation; hormone; signal
FEATURE      2-9      #region helix (right hand alpha)\
               15-25   #region helix (right hand alpha)
SUMMARY      #length 34 #molecular-weight 4128 #checksum 5508

Query Match  100.0%; Score 64; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.27e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 26 QDVHNFVAL 34
QY 1 QDVHNFVAL 9

Search completed: Thu Jul 30 10:52:17 1998
Job time : 26 secs.

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W E R E D (TW)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:50:38 1998; MasPar time 2.13 Seconds
106.097 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-23
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 QDVHNFVAL 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.654; Variance 24.782; scale 0.954

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	64	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	3.54e-04
2	64	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	3.54e-04
3	64	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	3.54e-04
4	64	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	3.54e-04
5	62	96.9	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.22e-03
6	49	76.6	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	2.17e+00
7	49	75.0	136	1	HYEP_RAT EPOXIDE HYDROLASE (EC	3.67e+00
8	48	75.0	153	1	Y441_MYCPN HYPOTHETICAL PROTEIN M	3.67e+00
9	48	75.0	153	1	M411_BRARE MELATONIN RECEPTOR TYP	3.67e+00
10	47	73.4	274	1	CDL_SYLFL T-CELL SURFACE GLYCOPR	6.15e+00
11	45	70.3	104	1	HYV2_LACHE HYPOTHETICAL 11.8 KD P	1.68e+01
12	45	70.3	252	1	TPIS_SCHJA TRIOSEPHOSPHATE ISOMER	1.68e+01
13	45	70.3	293	1	TPIS_SCHJA TRIOSEPHOSPHATE ISOMER	1.68e+01
14	45	70.3	257	1	YMY9_YEAST HYPOTHETICAL 34.0 KD P	1.68e+01
15	45	70.3	632	1	Y242_MYCPN HYPOTHETICAL PROTEIN M	1.68e+01
16	45	70.3	687	1	CSTA_HELPY CARBON STARVATION PROT	1.68e+01
17	45	70.3	917	1	SYL_STRAU ISOLEUCYL-TRNA SYNTHET	1.68e+01
18	45	70.3	2504	1	FAS_HUMAN FATTY ACID SYNTHASE (E	1.68e+01
19	45	70.3	2505	1	FAS_RAT FATTY ACID SYNTHASE (E	1.68e+01
20	44	68.8	227	1	UBI_DROME UBIQUITIN CARBOXYL-TER	2.75e+01
21	44	68.8	505	1	Y4XG_RHISN HYPOTHETICAL 55.5 KD P	2.75e+01
22	44	68.8	669	1	ACSA_PENCH ACETYL-COENZYME A SYNT	2.75e+01
23	44	68.8	670	1	ACSA_EMENT ACETYL-COENZYME A SYNT	2.75e+01

ID	PTHY_CANFA	STANDARD;	PRT;	115 AA.		
24	44	68.8	992	1	Y254_HUMAN HYPOTHETICAL PROTEIN K	2.75e+01
25	44	68.8	2133	1	FAS_FIG CONJUGATION FACTOR VII	2.75e+01
26	43	67.2	117	1	KVSH_MOUSE IG KAPPA CHAIN PRECURS	4.43e+01
27	43	67.2	219	1	RPIA_HAEN RIBOSE 5-PHOSPHATE ISO	4.43e+01
28	43	67.2	264	1	YOHG_BACSU HYPOTHETICAL 30.8 KD P	4.43e+01
29	43	67.2	302	1	D3D2_HUMAN 3,2-TRANS-ENOYL-COA IS	4.43e+01
30	43	67.2	309	1	VP62_MRDV PROBABLE NONSTRUCTURAL	4.43e+01
31	43	67.2	411	1	YIIB_ECOLI HYPOTHETICAL 45.7 KD P	4.43e+01
32	43	67.2	444	1	CADB_ECOLI PROBABLE CADDAVERINE/LY	4.43e+01
33	43	67.2	447	1	CLUS_RAT CLUSTERIN PRECURSOR (S	4.43e+01
34	43	67.2	449	1	CPFL_MACFA SERINE HYDROXYMETHYLTR	4.43e+01
35	43	67.2	483	1	CPQO_MESAU CYTOCHROME P450 IIC25	4.43e+01
36	43	67.2	490	1	CPQO_MESAU CYTOCHROME P450 IIC25	4.43e+01
37	43	67.2	490	1	CPQO_MESAU CYTOCHROME P450 IIC25	4.43e+01
38	43	67.2	490	1	CPQO_MESAU CYTOCHROME P450 IIC25	4.43e+01
39	43	67.2	493	1	CPQO_MESAU CYTOCHROME P450 IIC25	4.43e+01
40	43	67.2	493	1	CPQO_MESAU CYTOCHROME P450 IIC25	4.43e+01
41	43	67.2	741	1	CH12_YEAST CULLIN HOMOLOG 1 (CUL-	4.43e+01
42	43	67.2	752	1	YAXA_SCHPO HYPOTHETICAL 112.7 KD	4.43e+01
43	43	67.2	962	1	GLTB_SYNY3 FERREDOXIN-DEPENDENT G	4.43e+01
44	43	67.2	1550	1	GLTB_SYNY3 FERREDOXIN-DEPENDENT G	4.43e+01
45	43	67.2	2511	1	FAS_CHICK FATTY ACID SYNTHASE (E	4.43e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	115 AA.
ID	PTHY_CANFA	STANDARD;	PRT;	115 AA.
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUPHERIA; CARNIVORA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PARATHYROID;			
RX	MEDLINE; 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RA	DEWITTE J.W., CAPEN C.C.;			
RL	GENE 160:241-243(1995).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL; U15662; G558916; -			
DR	PROSITE; PS00335; PARATHYROID; 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL	1	25	BY SIMILARITY.
FT	PROPEP	26	31	BY SIMILARITY.
FT	CHAIN	32	115	PARATHYROID HORMONE.
SO	SEQUENCE	115 AA;	12957 MW;	16ED0BC CRC32;
Query Match				
Best Local Similarity 100.0%; Score 64; DB 1; Length 115;				
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
DB	60 QDVHNFVAL 68			
QY	1 QDVHNFVAL 9			
RESULT 2				
ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.
AC	P01268;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	BOS TAURUS (BOVINE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

Search completed: Thu Jul 30 10:50:45 1998
Job time : 7 secs.

```
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RN [2]
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RN [3]
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RN [4]
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RN [5]
RL GENE 28:319-329(1984).
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RN [6]
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RN [7]
RL AUBACH G.D., POTTS J.T. JR.;
RP HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RX MEDLINE; 71063634.
RA BREWER H.B. JR., ROMAN R.;
RN [8]
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RN [9]
RL DEFTOS L.J., DAWSON B.F., HOGAN M.L., AUBACH G.D.;
RP PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; J00106; G85; -
DR EMBL; J00023; G163641; -
DR EMBL; J00024; G163643; -
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K01938; G163647; -
DR EMBL; M25082; G163645; -
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 64; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3,54e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 60 QDVHNFVAL 68
QY 1 QDVHNFVAL 9
```

MUSEUM
(TM)

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Muscle_p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:51:03 1998; MasPar time 3.73 Seconds
101.507 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-23
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 QDVHNFVAL 9

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_invertebrate
13:sp_unclassified

Statistics: Mean 22.521; Variance 26.779; scale 0.841

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	52	81.3	105	10	PARATHYROID HORMONE (F	1.20e+00
2	52	81.3	345	9	STBA.	1.20e+00
3	49	76.6	207	11	ORE36L.	5.36e+00
4	49	76.6	455	10	MICROSOMAL EPOXIDE HYD	5.36e+00
5	48	75.0	117	11	GENOME, PARTIAL, SEQUEN	8.71e+00
6	48	75.0	377	3	T27A1.2 PROTEIN.	8.71e+00
7	46	71.9	535	8	BERBERINE BRIDGE ENZYM	2.25e+01
8	46	71.9	620	3	SIMILARITY TO MULTIPLE	2.25e+01
9	46	71.9	993	3	VINCULIN.	2.25e+01
10	45	70.3	163	9	PEPTIDYL-PROLYL CIS-TR	3.58e+01
11	45	70.3	552	9	POTASSIUM FLAVIN-ADENIN	3.58e+01
12	45	70.3	2509	10	FATTY ACID SYNTHASE. (E	3.58e+01
13	45	70.3	2509	2	FATTY ACID SYNTHASE. (E	3.58e+01
14	44	68.8	140	9	HYPOTHETICAL. 15.7 KD P	5.64e+01
15	44	68.8	155	12	OLFACTOR RECEPTOR (FR	5.64e+01
16	44	68.8	211	9	FROM BASES 2030342 TO	5.64e+01
17	44	68.8	255	9	TRIOSEPHOSPHATE ISOMER	5.64e+01
18	44	68.8	263	3	COSMID F48B9.	5.64e+01
19	44	68.8	315	10	VBETA2 PROTEIN.	5.64e+01
20	44	68.8	315	11	RETROVIRIDAE PROTEIN.	5.64e+01

RESULT ID	Score	Query Match	Length	DB ID	Description	Pred. No.
21	44	68.8	315	11	RETROVIRIDAE PROTEIN.	5.64e+01
22	44	68.8	326	9	HYPOTHETICAL. 36.0 KD P	5.64e+01
23	44	68.8	342	11	SIMILAR TO BACTERIOPHA	5.64e+01
24	44	68.8	368	3	SIMILAR TO S. CEREVISIA	5.64e+01
25	44	68.8	473	9	HYPOTHETICAL. 49.1 KD P	5.64e+01
26	44	68.8	491	1	ANALASE PRECURSOR.	5.64e+01
27	44	68.8	530	3	Z849.4.	5.64e+01
28	44	68.8	606	9	HD GAMMA.	5.64e+01
29	44	68.8	1221	3	K08E7.5.	5.64e+01
30	43	67.2	124	10	PRODUCT OF UNKNOWN FUN	8.83e+01
31	43	67.2	145	4	CYTOKROME P450 PB-1 (8.83e+01
32	43	67.2	169	10	CYTOKROME P450 PB-1 (8.83e+01
33	43	67.2	380	9	HYPOTHETICAL. 38.0 KD P	8.83e+01
34	43	67.2	387	3	T06D8.8.	8.83e+01
35	43	67.2	485	9	NDOH (FRAGMENT).	8.83e+01
36	43	67.2	490	10	CYTOKROME P450 IIC (E	8.83e+01
37	43	67.2	490	10	CYTOKROME P450 (EC 1.	8.83e+01
38	43	67.2	522	9	HYPOTHETICAL. 58.4 KD P	8.83e+01
39	43	67.2	565	8	GLUTATHIONE REDUCTASE	8.83e+01
40	43	67.2	760	12	ERCC2/XPD.	8.83e+01
41	43	67.2	886	12	ORIGIN RECOGNITION COM	8.83e+01
42	43	67.2	932	3	ZK250.6 PROTEIN.	8.83e+01
43	43	67.2	1283	3	SIMILAR TO MULTIDRUG-R	8.83e+01
44	43	67.2	2091	1	FATTY ACID SYNTHASE. B	8.83e+01
45	43	67.2	3083	11	POLYPROTEIN.	8.83e+01

ALIGNMENTS

RESULT ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	52	81.3	105	10	PARATHYROID HORMONE (F	1.20e+00
2	52	81.3	345	9	STBA.	1.20e+00
3	49	76.6	207	11	ORE36L.	5.36e+00
4	49	76.6	455	10	MICROSOMAL EPOXIDE HYD	5.36e+00
5	48	75.0	117	11	GENOME, PARTIAL, SEQUEN	8.71e+00
6	48	75.0	377	3	T27A1.2 PROTEIN.	8.71e+00
7	46	71.9	535	8	BERBERINE BRIDGE ENZYM	2.25e+01
8	46	71.9	620	3	SIMILARITY TO MULTIPLE	2.25e+01
9	46	71.9	993	3	VINCULIN.	2.25e+01
10	45	70.3	163	9	PEPTIDYL-PROLYL CIS-TR	3.58e+01
11	45	70.3	552	9	POTASSIUM FLAVIN-ADENIN	3.58e+01
12	45	70.3	2509	10	FATTY ACID SYNTHASE. (E	3.58e+01
13	45	70.3	2509	2	FATTY ACID SYNTHASE. (E	3.58e+01
14	44	68.8	140	9	HYPOTHETICAL. 15.7 KD P	5.64e+01
15	44	68.8	155	12	OLFACTOR RECEPTOR (FR	5.64e+01
16	44	68.8	211	9	FROM BASES 2030342 TO	5.64e+01
17	44	68.8	255	9	TRIOSEPHOSPHATE ISOMER	5.64e+01
18	44	68.8	263	3	COSMID F48B9.	5.64e+01
19	44	68.8	315	10	VBETA2 PROTEIN.	5.64e+01
20	44	68.8	315	11	RETROVIRIDAE PROTEIN.	5.64e+01

Thu Jul 30 13:38:06 1998

US-08-817-547A-23.ispt

Page 2

RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U59131; G1695865; -
KW P1ASMID.
SQ SEQUENCE 345 AA; 38433 MW; E194251E CRC32;

Query Match 81.3%; Score 52; DB 9; Length 345;
Best Local Similarity 77.8%; Pred. No. 1.20e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 116 ODVHLEFVL 124
||| ||:|
QY 1 ODVHNEVAL 9

Search completed: Thu Jul 30 10:51:32 1998
Job time : 29 secs.

WORLD

(TW)

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Masrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:55:02 1998; MasPar time 2.60 Seconds
47.193 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-24
Description: (1-8) from US08817547A.pep
Perfect Score: 57
Sequence: 1 DVHNFVAL 8

Scoring table:
PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.692; Variance 45.953; scale 0.341

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	57	100.0	38	9	R58151 [Ser22]-hPTH(1-38)-OH	5.52e+00
2	57	100.0	38	9	R58142 [Asn21]-hPTH(1-38)-OH	5.52e+00
3	57	100.0	38	9	R58140 [Phe21]-hPTH(1-38)-OH	5.52e+00
4	57	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	5.52e+00
5	57	100.0	38	9	R58133 [Asp19]-hPTH(1-38)-OH	5.52e+00
6	57	100.0	44	26	P30015 Human parathyroid hor	5.52e+00
7	57	100.0	47	25	W21946 Fusion protein compri	5.52e+00
8	57	100.0	84	27	W25687 Human parathyroid hor	5.52e+00
9	57	100.0	84	4	R23227 Human parathyroid hor	5.52e+00
10	57	100.0	84	4	R21181 Human parathyroid hor	5.52e+00
11	57	100.0	84	4	R23276 Bovine parathyroid ho	5.52e+00
12	57	100.0	84	4	R21254 Human parathyroid hor	5.52e+00
13	57	100.0	84	4	R23429 Porcine parathyroid h	5.52e+00
14	57	100.0	84	4	R23259 Bovine parathyroid h	5.52e+00
15	57	100.0	84	4	R23444 Porcine parathyroid h	5.52e+00
16	57	100.0	84	4	R23281 Bovine parathyroid ho	5.52e+00
17	57	100.0	84	4	R23424 Porcine parathyroid h	5.52e+00
18	57	100.0	84	4	R23383 Porcine parathyroid h	5.52e+00
19	57	100.0	84	4	R21161 Human parathyroid hor	5.52e+00

20	57	100.0	84	5	R29563 Oxidation resistant P	5.52e+00
21	57	100.0	84	4	R21241 Human parathyroid hor	5.52e+00
22	57	100.0	84	4	R21240 Human parathyroid hor	5.52e+00
23	57	100.0	84	25	W29420 Human parathyroid hor	5.52e+00
24	57	100.0	84	5	R29562 Oxidation resistant l	5.52e+00
25	57	100.0	84	5	R29561 Oxidation resistant P	5.52e+00
26	57	100.0	84	4	R23493 Porcine parathyroid h	5.52e+00
27	57	100.0	84	4	R23492 Porcine parathyroid h	5.52e+00
28	57	100.0	84	4	R23309 Bovine parathyroid ho	5.52e+00
29	57	100.0	84	4	R21199 Human parathyroid hor	5.52e+00
30	57	100.0	84	4	R21187 Human parathyroid hor	5.52e+00
31	57	100.0	84	4	R21219 Human parathyroid hor	5.52e+00
32	57	100.0	84	4	R21250 Human parathyroid hor	5.52e+00
33	57	100.0	84	4	R23248 Human parathyroid hor	5.52e+00
34	57	100.0	84	4	R23433 Porcine parathyroid h	5.52e+00
35	57	100.0	84	4	R23392 Porcine parathyroid h	5.52e+00
36	57	100.0	84	4	R23279 Bovine parathyroid ho	5.52e+00
37	57	100.0	84	4	R23278 Bovine parathyroid ho	5.52e+00
38	57	100.0	84	4	R23374 Bovine parathyroid ho	5.52e+00
39	57	100.0	84	4	R23240 Human parathyroid hor	5.52e+00
40	57	100.0	84	4	R23456 Porcine parathyroid h	5.52e+00
41	57	100.0	84	4	R23363 Bovine parathyroid ho	5.52e+00
42	57	100.0	84	4	R21210 Human parathyroid hor	5.52e+00
43	57	100.0	84	4	R21211 Human parathyroid hor	5.52e+00
44	57	100.0	84	4	R23449 Porcine parathyroid h	5.52e+00
45	57	100.0	229	9	R47971 Sequence of a full-le	5.52e+00

ALIGNMENTS

RESULT 1
ID R58151 standard; peptide; 38 AA.
AC R58151;
DT 20-SEP-1994 (first entry)
DE [Ser22]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PI 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANDOZ) SANDOZ LTD.
PA (BAUER) BAUER W.
PA (SANDOZ) SANDOZ PATENT GMBH.
PA (SANDOZ) SANDOZ-ERFINDUNG VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage F, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 148, page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA:

Query Match 100.0%; Score 57; DB 9; Length 38;
Best local similarity 100.0%; Pred. No. 5.52e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 30 dvhnfval 37

OY 1 DVHNFVAL 8

RESULT 2
ID R58142 standard; peptide: 38 AA.

AC R58142;
DE 20-SEP-1994 (first entry)
DE [Asn21]-hPTH(1-38)-OH
KW Human parathyroid hormone; hPTH; variant; analogue;
KW Calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.

PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.

PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ-PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 139, Page 40: 92pp: English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 57; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.52e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 30 dvhmfval 37
1 DVHNFVAL 8

Search completed: Thu Jul 30 10:55:16 1998
Job time : 14 secs.

M P S R C H
***** (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:54:14 1998; Maspar time 3.34 Seconds
Tabular output not generated. 87.598 Million cell updates/sec

Title: >US-08-817-547A-24
Description: (1-8) from US08817547A.pep
Perfect Score: 57
Sequence: 1 DVHNFVAL 8

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 21.941; Variance 28.147; scale 0.780

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	57	100.0	34	5 12WE	parathyroid hormone (1.14e-01	
2	57	100.0	34	5 12WE	parathyroid hormone (1.14e-01	
3	57	100.0	34	5 12WE	parathyroid hormone (1.14e-01	
4	57	100.0	35	5 12WD	parathyroid hormone (1.14e-01	
5	57	100.0	36	5 12WB	parathyroid hormone (1.14e-01	
6	57	100.0	37	5 12WB	parathyroid hormone (1.14e-01	
7	57	100.0	37	5 12WB	parathyroid hormone (1.14e-01	
8	57	100.0	37	5 12WB	parathyroid hormone (1.14e-01	
9	57	100.0	115	1 PTRU	parathyroid hormone p 1.14e-01	
10	57	100.0	115	1 PTRU	parathyroid hormone p 1.14e-01	
11	57	100.0	115	1 PTRU	parathyroid hormone p 1.14e-01	
12	55	96.5	115	1 PTRU	parathyroid hormone p 1.14e-01	
13	47	82.5	136	2 S73520	parathyroid hormone p 3.12e-01	
14	46	80.7	201	2 C65188	MG441 homolog E09-ort 1.39e+01	
15	46	80.7	274	2 B45887	hypothetical 22.3 kd 2.18e+01	
16	46	80.7	1520	2 G69634	leukocyte differential 2.18e+01	
17	46	78.9	104	2 B37145	glutamate synthase (1 3.39e+01	
18	45	78.9	105	2 B37145	hypothetical 12k hlv 3.39e+01	
19	45	78.9	105	2 B37145	hypothetical 12k hlv 3.39e+01	
20	45	78.9	297	2 S55085	parathyroid hormone - 3.39e+01	
21	45	78.9	687	2 H64665	carbon starvation pro 3.39e+01	
22	45	78.9	2504	2 B57788	fatty-acid synthase (3.39e+01	
23	45	78.9	2504	2 A57788	fatty-acid synthase (3.39e+01	
24	45	76.9	2505	1 XYRTFA	fatty-acid synthase (3.39e+01	

24	45	78.9	2509	2 G01890	fatty-acid synthase (3.39e+01
25	44	77.2	140	2 A69445	hypothetical protein 5.24e+01
26	44	77.2	227	2 S33956	ubiquitin thiolesterase 5.24e+01
27	44	77.2	632	2 S73824	MG242 homolog H91.ort 5.24e+01
28	43	75.4	219	2 B64153	ribose-5-phosphate is 8.03e+01
29	43	75.4	302	2 A55723	dodecenoyl-CoA Delta- 8.03e+01
30	43	75.4	309	2 B38545	hypothetical protein 8.03e+01
31	43	75.4	444	2 A41842	lysine/cadaverine ant 8.03e+01
32	43	75.4	760	2 I51720	probable DNA helicase 8.03e+01
33	43	75.4	962	2 S67385	hypothetical protein 8.03e+01
34	43	75.4	2512	1 XYCHFA	fatty-acid synthase (8.03e+01
35	42	73.7	178	5 1CTNA	cyclophilin b, chain 1.22e+02
36	42	73.7	182	5 2RMCE	cyclophilin c complex 1.22e+02
37	42	73.7	182	5 2RMCC	cyclophilin c complex 1.22e+02
38	42	73.7	182	5 2RMCG	cyclophilin c complex 1.22e+02
39	42	73.7	182	5 2RMCA	cyclophilin c complex 1.22e+02
40	42	73.7	207	2 A40516	peptidylprolyl isomer 1.22e+02
41	42	73.7	208	1 CSHUB	peptidylprolyl isomer 1.22e+02
42	42	73.7	212	2 A40047	peptidylprolyl isomer 1.22e+02
43	42	73.7	212	2 A54204	peptidylprolyl isomer 1.22e+02
44	42	73.7	316	2 S07569	protein H5 - slime mo 1.22e+02
45	42	73.7	1321	2 S27337	multidrug resistance 1.22e+02

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	
KEYWORDS		hormone	
FEATURE			
15-25			
SUMMARY		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 57; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.14e-01;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	27	DVHNFVAL 34	
QY	1	DVHNFVAL 8	
RESULT	2	12WG	#type complete
ENTRY		parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-1-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		TN003319	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 2-9 #region helix (right hand alpha)\
 15-25 #region helix (right hand alpha)
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 57; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1,14e-01;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 DVHNFVAL 34
 |||||
 QY 1 DVHNFVAL 8

Search completed: Thu Jul 30 10:54:45 1998
 Job time : 31 secs.

Search completed: Thu Jul 30 10:53:13 1998
Job time : 6 secs.

```
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T., JR., RICH A.; U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.; U.S.A. 78:4073-4077(1981).
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.; U.S.A. 78:4073-4077(1981).
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RL COHN D.V.; U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RL AUBRACH G.D., POTTS J.T., JR.; U.S.A. 68:63-67(1971).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREWER H.B., JR., ROMAN R.; U.S.A. 67:1862-1869(1970).
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFTOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.; U.S.A. 68:63-67(1971).
RN [9]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
RL BONE AND PREVENTING THEIR RENAL EXCRETION.
RN [10]
RP EMBL: 000106; G85; -.
RX EMBL: 000023; G163641; -.
RL EMBL: 000024; G163643; -.
RN [11]
RP EMBL: 000024; E18249; ALT_SEQ.
RX EMBL: 000024; E18250; ALT_INIT.
RL EMBL: K01938; G163647; -.
RN [12]
RP EMBL: M25082; G163645; -.
RX PIR: A01534; PTBO.
RL PIR: A24949; A24949.
RN [13]
RP PROSITE: PS00335; PARATHYROID: 1.
RX HORMONE; SIGNAL.
RL SIGNAL.
RN [14]
RP PROPEP 26 31
RX CHAIN 32 115 PARATHYROID HORMONE.
RL CONFLICT 106 106 V -> G (IN REF. 4).
RN [15]
RP SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;
RX QUERY MATCH 100.0%; Score 57; DB 1; Length 115;
RL BEST LOCAL SIMILARITY 100.0%; Pred. No. 8.14e-03;
RN MATCHES 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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MOL

(TW)

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MPSrch_DP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:53:31 1998; MasPar time 3.69 Seconds
Tabular output not generated. 91.336 Million cell updates/sec

Title: >US-08-817-547A-24
Description: (1-8) from US08817547A.pep
Perfect Score: 57
Sequence: 1 DVHNFVAL 8

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: strepmb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.944; Variance 25.449; scale 0.862

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	46	80.7	620	3	001909	SIMILARITY TO MULTIPLE PARATHYROID HORMONE (F STB).	1.28e+01
2	45	78.9	105	10	063473	PUTATIVE FLAVELLA-RELA	2.08e+01
3	45	78.9	345	9	P95793	FATTY ACID SYNTHASE (E	2.08e+01
4	45	78.9	552	9	O06642	FATTY ACID SYNTHASE (E	2.08e+01
5	45	78.9	2509	10	063577	GENOME, PARTIAL SEQUEN	3.35e+01
6	45	78.9	2509	2	016702	HYPOHETICAL 15.7 KD P	3.35e+01
7	44	77.2	117	11	084562	SIMILAR TO S. CEREVISI	3.35e+01
8	44	77.2	140	9	028710	HYPOHETICAL 49.1 KD P	3.35e+01
9	44	77.2	368	9	021158	DELTA3, DELTA-ENOMYL-C	5.35e+01
10	44	77.2	473	9	024723	ERCC2/XPD.	5.35e+01
11	43	75.4	266	2	013290	ERCC2/XPD.	5.35e+01
12	43	75.4	760	12	091941	ERCC2/XPD.	5.35e+01
13	43	75.4	932	3	017301	ERCC2/XPD.	5.35e+01
14	43	75.4	1221	3	021344	K08E7.5.	5.35e+01
15	43	75.4	1283	3	018824	SIMILAR TO MUTIFRUG-R	5.35e+01
16	43	75.4	2408	2	092566	MYELOBLAST KIA0279 (F	5.35e+01
17	42	73.7	62	9	P76618	FROM BASES 27575730 TO	8.47e+01
18	42	73.7	195	9	049043	ABC TRANSPORTER (OLIGO	8.47e+01
19	42	73.7	196	3	094770	CYCLOPHILIN HOMOLOG TA	8.47e+01
20	42	73.7	207	11	039628	ORF36L.	8.47e+01

RESULT	1	PRELIMINARY:	PRT:	620 AA.
ID	001909			
AC	001909;			
DT	01-JUL-1997 (TREMBLREL. 04, CREATED)			
DT	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)			
DT	01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)			
DE	SIMILARITY TO MULTIPLE CADHERIN-TYPE REPEATS.			
GN	K10F2.2.			
OS	CENOMADITIS ELEGANS.			
OC	EKAROTIA; METAFOA; ACCELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RX	MEDLINE; 94150718.			
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,			
RA	BOFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,			
RA	CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELL A., FULTON L.,			
RA	GARDNER A., GREEN P., HAWKINS T., HILLER L., JIRI M., JOHNSTON L.,			
RA	JONES M., KERSHAW J., KIRSTEN J., LAISNER N., LATREILLE P.,			
RA	LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,			
RA	PARSONS J., PERCY C., RIEREN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,			
RA	SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,			
RA	THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,			
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,			
RL	NATURE 368:32-38(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RA	DU Z., GATTUNG S.;			
RL	SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RA	WATERSTON R.;			
RL	SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL: AF003388; G2088851; -			
SO	SEQUENCE 620 AA; 67475 MW; 17C581A5 CRC32;			

ALIGNMENTS

Query Match: 80.7%; Score 46; DB 3; Length 620;
Best Local Similarity 75.0%; Pred. No. 1.28e+01;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 134 DVHNFVAL 141
||| |||

OY 1 DVHNFVAL 8

RESULT 2
ID 063473 PRELIMINARY; PRT; 105 AA.

AC 063473;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE PARATHYROID HORMONE (FRAGMENT).

GN PTH.

OS RATIUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-THYROID, AND PARATHYROID;

RA SCHMELZER H.J., GROSS G., MAYER H.;

RL ADV. GENE TECHNOL. 21:228-229(1984).

EMBL: M54875; G601933; -.

NON_TER 1
SEQUENCE 105 AA; 11746 MM; 6AC3163E CRC32;

Query Match 78.9%; Score 45; DB 10; Length 105;

Best Local Similarity 75.0%; Pred. No. 2.08e+01;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 51 DGHNFVSL 58
OY 1 DVHNFVAL 8

Search completed: Thu Jul 30 10:53:58 1998
Job time : 27 secs.

OY 1 VHNFEVAL 7

RESULT 2
ID R58128 standard; peptide: 38 AA.
AC R58128; 20-SEP-1994 (first entry)
DE [His19]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteoporosis;
hypoparathyroidism.
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384
PR 15-JUL-1992; GB-013009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
28-JAN-1993; GB-001691.
28-JAN-1993; GB-001692.
14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
Waelchli R, Rainer A;
PI MPI; 94-018352/03.
DR New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc. English.
PS Example 126; Page 39; 92pp; English.
CC This peptide is an example of a highly generic formula covering
parathyroid hormone variants useful for treating or preventing bone
conditions associated with calcium depletion/resorption, in cases
where calcium fixation is required (esp. osteoporosis) or to treat
hypoparathyroidism.
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 51; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.64e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 vhnfeval 37
1 VHNFEVAL 7

Search completed: Thu Jul 30 10:57:31 1998
Job time : 14 secs.

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(TM)

Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:56:41 1998; MasPar time 3.23 Seconds
Tabular output not generated. 79.088 Million cell updates/sec

Title: >US-08-817-547A-25
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 VHNFEVAL 7

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nrl3d

Statistics: Mean 21.152; Variance 25.908; scale 0.816

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	51	100.0	34	5	12WE parathyroid hormone (7.97e-01	
2	51	100.0	34	5	12WE parathyroid hormone (7.97e-01	
3	51	100.0	34	5	12WE parathyroid hormone (7.97e-01	
4	51	100.0	35	5	12WE parathyroid hormone (7.97e-01	
5	51	100.0	36	5	12WE parathyroid hormone (7.97e-01	
6	51	100.0	37	5	12WE parathyroid hormone (7.97e-01	
7	51	100.0	37	5	12WE parathyroid hormone (7.97e-01	
8	51	100.0	115	1	PTHU parathyroid hormone (7.97e-01	
9	51	100.0	115	2	JC4202 parathyroid hormone (7.97e-01	
10	51	100.0	115	1	PRBG parathyroid hormone (7.97e-01	
11	51	100.0	115	1	PRBO parathyroid hormone (7.97e-01	
12	49	96.1	115	1	A05091 parathyroid hormone (2.18e+00	
13	46	90.2	136	2	S73520 MG441 homolog E09_crf 9.40e+00	
14	46	90.2	201	2	C65188 hypothetical 22.3 kd 9.40e+00	
15	45	88.2	297	2	S55085 hypothetical protein 1.51e+01	
16	45	88.2	687	2	H64665 carbon starvation pro 1.51e+01	
17	45	88.2	2504	2	B57788 fatty acid synthase (1.51e+01	
18	45	88.2	2504	2	A57788 fatty acid synthase (1.51e+01	
19	45	88.2	2505	1	XYRTFA fatty acid synthase (1.51e+01	
20	44	88.2	2509	2	G01880 fatty acid synthase (1.51e+01	
21	44	86.3	227	2	S33956 ubiquitin thiolester (2.41e+01	
22	43	84.3	2512	1	XYCHFA fatty acid synthase (3.61e+01	
23	42	82.4	46	2	S45724 peptidylprolyl isomer 5.98e+01	

24	42	82.4	87	2	S21218	peptidylprolyl isomer	5.98e+01
25 <td>42<td>82.4<td>105<td>2<td>I51851<td>parathyroid hormone -</td><td>5.98e+01</td></td></td></td></td></td>	42 <td>82.4<td>105<td>2<td>I51851<td>parathyroid hormone -</td><td>5.98e+01</td></td></td></td></td>	82.4 <td>105<td>2<td>I51851<td>parathyroid hormone -</td><td>5.98e+01</td></td></td></td>	105 <td>2<td>I51851<td>parathyroid hormone -</td><td>5.98e+01</td></td></td>	2 <td>I51851<td>parathyroid hormone -</td><td>5.98e+01</td></td>	I51851 <td>parathyroid hormone -</td> <td>5.98e+01</td>	parathyroid hormone -	5.98e+01
26 <td>42<td>82.4<td>178<td>5</td><td>1CYNA</td><td>cyclophilin b, chain</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>178<td>5</td><td>1CYNA</td><td>cyclophilin b, chain</td><td>5.98e+01</td></td></td>	82.4 <td>178<td>5</td><td>1CYNA</td><td>cyclophilin b, chain</td><td>5.98e+01</td></td>	178 <td>5</td> <td>1CYNA</td> <td>cyclophilin b, chain</td> <td>5.98e+01</td>	5	1CYNA	cyclophilin b, chain	5.98e+01
27 <td>42<td>82.4<td>182<td>5</td><td>2RMCE</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>182<td>5</td><td>2RMCE</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td>	82.4 <td>182<td>5</td><td>2RMCE</td><td>cyclophilin c complex</td><td>5.98e+01</td></td>	182 <td>5</td> <td>2RMCE</td> <td>cyclophilin c complex</td> <td>5.98e+01</td>	5	2RMCE	cyclophilin c complex	5.98e+01
28 <td>42<td>82.4<td>182<td>5</td><td>2RMCC</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>182<td>5</td><td>2RMCC</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td>	82.4 <td>182<td>5</td><td>2RMCC</td><td>cyclophilin c complex</td><td>5.98e+01</td></td>	182 <td>5</td> <td>2RMCC</td> <td>cyclophilin c complex</td> <td>5.98e+01</td>	5	2RMCC	cyclophilin c complex	5.98e+01
29 <td>42<td>82.4<td>182<td>5</td><td>2RMCG</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>182<td>5</td><td>2RMCG</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td>	82.4 <td>182<td>5</td><td>2RMCG</td><td>cyclophilin c complex</td><td>5.98e+01</td></td>	182 <td>5</td> <td>2RMCG</td> <td>cyclophilin c complex</td> <td>5.98e+01</td>	5	2RMCG	cyclophilin c complex	5.98e+01
30 <td>42<td>82.4<td>182<td>5</td><td>2RMCA</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>182<td>5</td><td>2RMCA</td><td>cyclophilin c complex</td><td>5.98e+01</td></td></td>	82.4 <td>182<td>5</td><td>2RMCA</td><td>cyclophilin c complex</td><td>5.98e+01</td></td>	182 <td>5</td> <td>2RMCA</td> <td>cyclophilin c complex</td> <td>5.98e+01</td>	5	2RMCA	cyclophilin c complex	5.98e+01
31 <td>42<td>82.4<td>183<td>2</td><td>S71547</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>183<td>2</td><td>S71547</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td>	82.4 <td>183<td>2</td><td>S71547</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td>	183 <td>2</td> <td>S71547</td> <td>peptidylprolyl isomer</td> <td>5.98e+01</td>	2	S71547	peptidylprolyl isomer	5.98e+01
32 <td>42<td>82.4<td>207</td><td>2</td><td>A40516</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td>	42 <td>82.4<td>207</td><td>2</td><td>A40516</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td>	82.4 <td>207</td> <td>2</td> <td>A40516</td> <td>peptidylprolyl isomer</td> <td>5.98e+01</td>	207	2	A40516	peptidylprolyl isomer	5.98e+01
33 <td>42<td>82.4<td>208<td>1</td><td>CSHUB</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>208<td>1</td><td>CSHUB</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td>	82.4 <td>208<td>1</td><td>CSHUB</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td>	208 <td>1</td> <td>CSHUB</td> <td>peptidylprolyl isomer</td> <td>5.98e+01</td>	1	CSHUB	peptidylprolyl isomer	5.98e+01
34 <td>42<td>82.4<td>212<td>2</td><td>A54204</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>212<td>2</td><td>A54204</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td>	82.4 <td>212<td>2</td><td>A54204</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td>	212 <td>2</td> <td>A54204</td> <td>peptidylprolyl isomer</td> <td>5.98e+01</td>	2	A54204	peptidylprolyl isomer	5.98e+01
35 <td>42<td>82.4<td>212<td>2</td><td>A40047</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>212<td>2</td><td>A40047</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td>	82.4 <td>212<td>2</td><td>A40047</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td>	212 <td>2</td> <td>A40047</td> <td>peptidylprolyl isomer</td> <td>5.98e+01</td>	2	A40047	peptidylprolyl isomer	5.98e+01
36 <td>42<td>82.4<td>216<td>2</td><td>A56861</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>216<td>2</td><td>A56861</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td></td>	82.4 <td>216<td>2</td><td>A56861</td><td>peptidylprolyl isomer</td><td>5.98e+01</td></td>	216 <td>2</td> <td>A56861</td> <td>peptidylprolyl isomer</td> <td>5.98e+01</td>	2	A56861	peptidylprolyl isomer	5.98e+01
37 <td>42<td>82.4<td>316<td>2</td><td>S07569</td><td>protein H5 - slime mo</td><td>5.98e+01</td></td></td></td>	42 <td>82.4<td>316<td>2</td><td>S07569</td><td>protein H5 - slime mo</td><td>5.98e+01</td></td></td>	82.4 <td>316<td>2</td><td>S07569</td><td>protein H5 - slime mo</td><td>5.98e+01</td></td>	316 <td>2</td> <td>S07569</td> <td>protein H5 - slime mo</td> <td>5.98e+01</td>	2	S07569	protein H5 - slime mo	5.98e+01
38 <td>42<td>82.4<td>541</td><td>2</td><td>A25696</td><td>yellow protein - fru1</td><td>5.98e+01</td></td></td>	42 <td>82.4<td>541</td><td>2</td><td>A25696</td><td>yellow protein - fru1</td><td>5.98e+01</td></td>	82.4 <td>541</td> <td>2</td> <td>A25696</td> <td>yellow protein - fru1</td> <td>5.98e+01</td>	541	2	A25696	yellow protein - fru1	5.98e+01
39 <td>42<td>82.4<td>672</td><td>2</td><td>S46276</td><td>acetate--CoA ligase (</td><td>5.98e+01</td></td></td>	42 <td>82.4<td>672</td><td>2</td><td>S46276</td><td>acetate--CoA ligase (</td><td>5.98e+01</td></td>	82.4 <td>672</td> <td>2</td> <td>S46276</td> <td>acetate--CoA ligase (</td> <td>5.98e+01</td>	672	2	S46276	acetate--CoA ligase (5.98e+01
40 <td>41<td>80.4<td>537</td><td>2</td><td>S67434</td><td>hypothetical protein</td><td>9.32e+01</td></td></td>	41 <td>80.4<td>537</td><td>2</td><td>S67434</td><td>hypothetical protein</td><td>9.32e+01</td></td>	80.4 <td>537</td> <td>2</td> <td>S67434</td> <td>hypothetical protein</td> <td>9.32e+01</td>	537	2	S67434	hypothetical protein	9.32e+01
41 <td>41<td>80.4<td>599</td><td>2</td><td>S18612</td><td>lipoxigenase (EC 1.13</td><td>9.32e+01</td></td></td>	41 <td>80.4<td>599</td><td>2</td><td>S18612</td><td>lipoxigenase (EC 1.13</td><td>9.32e+01</td></td>	80.4 <td>599</td> <td>2</td> <td>S18612</td> <td>lipoxigenase (EC 1.13</td> <td>9.32e+01</td>	599	2	S18612	lipoxigenase (EC 1.13	9.32e+01
42 <td>41<td>80.4<td>632</td><td>2</td><td>S73824</td><td>MG242 homolog H81_crf</td><td>9.32e+01</td></td></td>	41 <td>80.4<td>632</td><td>2</td><td>S73824</td><td>MG242 homolog H81_crf</td><td>9.32e+01</td></td>	80.4 <td>632</td> <td>2</td> <td>S73824</td> <td>MG242 homolog H81_crf</td> <td>9.32e+01</td>	632	2	S73824	MG242 homolog H81_crf	9.32e+01
43 <td>41<td>80.4<td>864</td><td>2</td><td>S13381</td><td>lipoxigenase (EC 1.13</td><td>9.32e+01</td></td></td>	41 <td>80.4<td>864</td><td>2</td><td>S13381</td><td>lipoxigenase (EC 1.13</td><td>9.32e+01</td></td>	80.4 <td>864</td> <td>2</td> <td>S13381</td> <td>lipoxigenase (EC 1.13</td> <td>9.32e+01</td>	864	2	S13381	lipoxigenase (EC 1.13	9.32e+01
44 <td>41<td>80.4<td>924</td><td>2</td><td>S34926</td><td>hypothetical protein</td><td>9.32e+01</td></td></td>	41 <td>80.4<td>924</td><td>2</td><td>S34926</td><td>hypothetical protein</td><td>9.32e+01</td></td>	80.4 <td>924</td> <td>2</td> <td>S34926</td> <td>hypothetical protein</td> <td>9.32e+01</td>	924	2	S34926	hypothetical protein	9.32e+01
45 <td>41<td>80.4<td>1520</td><td>2</td><td>G69634</td><td>glutamate synthase (1</td><td>9.32e+01</td></td></td>	41 <td>80.4<td>1520</td><td>2</td><td>G69634</td><td>glutamate synthase (1</td><td>9.32e+01</td></td>	80.4 <td>1520</td> <td>2</td> <td>G69634</td> <td>glutamate synthase (1</td> <td>9.32e+01</td>	1520	2	G69634	glutamate synthase (1	9.32e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE			
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#book		Marx, U.C.	
COMMENT		In Strukturen Verschiedener Parathormonfragmente In Loesung,	
COMMENT		pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
KEYWORDS		Resolution: not applicable	
FEATURE		hormone	
SUMMARY		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 51; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 7.97e-01;	
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	28	VHNFEVAL 34	
Qy	1	VHNFEVAL 7	
RESULT	2	12WE	#type complete
ENTRY		parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN003319	
#book		Marx, U.C.	
COMMENT		In Strukturen Verschiedener Parathormonfragmente In Loesung,	
COMMENT		pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
		Resolution: not applicable	

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 2-9 #region helix (right hand alpha)\
 15-25 #region helix (right hand alpha)
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 51; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.97e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 28 VHNFEVAL 34
 QY 1 VHNFEVAL 7

Search completed: Thu Jul 30 10:57:00 1998
 Job time : 19 secs.

WORLDWIDE
(TW)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:55:35 1998; MasPar time 2.08 Seconds
Tabular output not generated. 84.457 Million cell updates/sec

Title: >US-08-817-547A-25
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 VHNFEVAL 7

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.139; Variance 21.222; scale 1.043

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description	Pred. No.
1	51	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	8.19e-02
2	51	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	8.19e-02
3	51	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	8.19e-02
4	51	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	8.19e-02
5	49	96.1	115	1	PTHY_RAT PARATHYROID HORMONE PR	2.80e-01
6	46	90.2	136	1	Y441_MYCPN HYPOTHETICAL PROTEIN M	1.66e+00
7	46	90.2	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	1.66e+00
8	45	88.2	297	1	YMY9_YEAST HYPOTHETICAL 34.0 KD P	2.95e+00
9	45	88.2	687	1	CSTA_HELPY CARBON STARVATION PROT	2.95e+00
10	45	88.2	2504	1	FAS_HUMAN FATTY ACID SYNTHASE (E	2.95e+00
11	45	88.2	2505	1	FAS_RAT FATTY ACID SYNTHASE (E	2.95e+00
12	44	86.3	227	1	UBI_DRONE UBIQUITIN CARBOXYL-TER	5.18e+00
13	44	86.3	505	1	Y4XG_RHISM HYPOTHETICAL 55.5 KD P	5.18e+00
14	43	84.3	752	1	CUL1_HUMAN CULIN HOMOLOG 1 (CUL-	9.02e+00
15	43	84.3	2511	1	FAS_CHICK FATTY ACID SYNTHASE (E	9.02e+00
16	42	82.4	161	1	YCK5_EUGGR HYPOTHETICAL 18.6 KD P	1.55e+01
17	42	82.4	207	1	CYBP_CHICK PEPTIDYL-PROLYL CIS-TR	1.55e+01
18	42	82.4	208	1	CYBP_RAT PEPTIDYL-PROLYL CIS-TR	1.55e+01
19	42	82.4	208	1	CYBP_HUMAN PEPTIDYL-PROLYL CIS-TR	1.55e+01
20	42	82.4	208	1	CYBP_MOUSE PEPTIDYL-PROLYL CIS-TR	1.55e+01
21	42	82.4	208	1	CYBP_BOVIN PEPTIDYL-PROLYL CIS-TR	1.55e+01
22	42	82.4	212	1	CYPC_HUMAN PEPTIDYL-PROLYL CIS-TR	1.55e+01
23	42	82.4	212	1	CYPC_MOUSE PEPTIDYL-PROLYL CIS-TR	1.55e+01

24	42	82.4	316	1	VSH5_DICDI VEGETATIVE SPECIFIC PR	1.55e+01
25	42	82.4	541	1	YELL_DRONE YELLOW PROTEIN.	1.55e+01
26	41	80.4	537	1	AREH_SCHPO PROBABLE STEROL O-ACYL	2.64e+01
27	41	80.4	632	1	Y242_MYCPN HYPOTHETICAL PROTEIN M	2.64e+01
28	41	80.4	864	1	LOXX_SOYBN SEED LIPOXYGENASE (EC	2.64e+01
29	41	80.4	924	1	YB53_YEAST HYPOTHETICAL 104.5 KD	2.64e+01
30	40	78.4	216	1	Y886_CABEL HYPOTHETICAL 23.9 KD P	4.45e+01
31	40	78.4	274	1	CD1_STLFL T-CELL SURFACE GLYCOPR	4.45e+01
32	40	78.4	408	1	GPT_CRIGR UDP-N-ACETYLGLUCOSAMIN	4.45e+01
33	40	78.4	408	1	GPT_CRILLO UDP-N-ACETYLGLUCOSAMIN	4.45e+01
34	40	78.4	430	1	BMP7_MOUSE BONE MORPHOGENETIC PRO	4.45e+01
35	40	78.4	431	1	BMP7_HUMAN BONE MORPHOGENETIC PRO	4.45e+01
36	40	78.4	444	1	CADB_ECOLI PROBABLE CADYERINE/LY	4.45e+01
37	40	78.4	507	1	LCK_CHICK PROTO-ONCOGENE TYROSIN	4.45e+01
38	40	78.4	578	1	YFPA_ECOLI HYPOTHETICAL 64.5 KD P	4.45e+01
39	40	78.4	607	1	UGST_SOLU GRANULE-BOUND GLYCOSEN	4.45e+01
40	40	78.4	782	1	ZFY1_MOUSE ZINC FINGER Y-CHROMOSO	4.45e+01
41	40	78.4	783	1	ZFY2_MOUSE ZINC FINGER Y-CHROMOSO	4.45e+01
42	40	78.4	801	1	ZFY_HUMAN ZINC FINGER X-CHROMOSO	4.45e+01
43	40	78.4	805	1	ZFX_HUMAN ZINC FINGER X-CHROMOSO	4.45e+01
44	40	78.4	805	1	SEC6_YEAST EXOCYST COMPLEX COMPON	4.45e+01
45	40	78.4	847	1	ENV_HVIW2 ENVELOPE POLYPROTEIN G	4.45e+01

ALIGNMENTS

RESULT	1	PTHY_CANFA	STANDARD;	PRT;	115 AA.
AC	P52212;				
DT	01-OCT-1996 (REL. 34, CREATED)				
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	CANIS FAMILIARIS (DOG).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUHETERIA; CARNIVORA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PARATHYROID;				
RX	MEDLINE; 95369696.				
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A., DEWITTE J.W., CAPEN C.C., GENE 160:241-243(1995).				
RL	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN				
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.				
CC	EMBL; U15662; G558916; -.				
DR	PROSITE; PS00335; PARATHYROID; 1.				
DR	KR HORMONE; SIGNAL.				
FT	SIGNAL.				
FT	PROPEP				
FT	CHAIN				
SQ	SEQUENCE 115 AA; 12957 MW; 16DEDEBC CRC32;				
Query Match					
Best Local Similarity	100.0%;	Score 51;	DB 1;	length 115;	
Matches	7;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Db	62 VHNFEVAL 68				
Qy	1 VHNFEVAL 7				
RESULT	2				
ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.	
AC	P01268;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				

Search completed: Thu Jul 30 10:55:41 1998
Job time : 6 secs.

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZUB J.A., NATHANS J., SHARP P.A.,
RA POTTS J.T., JR., RICH A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RA COHN D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RA AURBACH G.D., POTTS J.T., JR.;
RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREWER H.B., JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEFTOS T.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; V00106; G85; -.
DR EMBL; J00023; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K01938; G163647; -.
DR EMBL; M25082; G163645; -.
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V->G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EASF2 CRC32;

Query Match 100.0%; Score 51; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8,198-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 62 VHNFEVAL 68
OY 1 VHNFEVAL 7

WIDEOR (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:55:58 1998; Maspar time 3.65 Seconds
Tabular output not generated. 80.757 Million cell updates/sec

Title: >US-08-817-547A-25
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 VHNFFVAL 7

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.229; Variance 23.108; scale 0.919

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	45	88.2	2505	10	063577	FATTY ACID SYNTHASE. 7.93e+00
2	45	88.2	2509	2	016702	FATTY ACID SYNTHASE (E 7.93e+00
3	44	86.3	368	3	021158	SIMILAR TO S. CERVISIAE 1.33e+01
4	43	84.3	1221	3	021344	KOBE7.5. 2.22e+01
5	42	82.4	105	10	063473	PARATHYROID HORMONE (F 3.67e+01
6	42	82.4	196	3	094770	CYCLOPHILIN HOMOLOG TA 3.67e+01
7	42	82.4	284	3	094311	SIMILARITY TO EGF-LIKE 3.67e+01
8	42	82.4	485	9	P95169	NUOM (FRAGMENT). 3.67e+01
9	42	82.4	535	8	P93479	BERBERINE BRIDGE ENZY 3.67e+01
10	42	82.4	568	3	002437	YELLOW. 3.67e+01
11	42	82.4	672	1	001576	ACETYL-COA SYNTHETASE. 3.67e+01
12	42	82.4	932	1	017301	ZK250.6 PROTEIN. 3.67e+01
13	42	82.4	2408	2	092566	MYELOBLAST KIA00279 (F 3.67e+01
14	41	80.4	117	11	084562	GENOME, PARTIAL SEQUE 6.00e+01
15	41	80.4	326	3	017775	F09C3.4. 6.00e+01
16	41	80.4	378	3	P91080	COSMID C23h3. 6.00e+01
17	41	80.4	530	3	018303	ZK849.4. 6.00e+01
18	41	80.4	599	8	041244	LIPIDOMYXINASE. 6.00e+01
19	41	80.4	645	3	002261	F44P1.5. 6.00e+01
20	41	80.4	1149	3	023315	ZC434.5. 6.00e+01

21	41	80.4	1774	3	093636	F29G6.3B. 6.00e+01
22	41	80.4	1903	1	P87204	FKSP PROTEIN INVOLVED 6.00e+01
23	41	80.4	1918	3	093637	F29G6.3A. 6.00e+01
24	40	78.4	90	11	072849	ENVELOPE GLYCOPROTEIN 9.72e+01
25	40	78.4	91	11	072852	ENVELOPE GLYCOPROTEIN 9.72e+01
26	40	78.4	91	11	072856	ENVELOPE GLYCOPROTEIN 9.72e+01
27	40	78.4	91	11	072854	ENVELOPE GLYCOPROTEIN 9.72e+01
28	40	78.4	115	6	033000	ORE115. 9.72e+01
29	40	78.4	175	9	P77949	CYCLOPHILIN SCYPB (EC 9.72e+01
30	40	78.4	256	6	004315	HYPOHETICAL 20.0 KD P 9.72e+01
31	40	78.4	296	9	P76472	FROM BASES 2360084 TO 9.72e+01
32	40	78.4	400	2	015216	GLCNAC-1-P TRANSFERASE 9.72e+01
33	40	78.4	460	9	051510	PROTEIN E1 PRECURSOR. 9.72e+01
34	40	78.4	488	9	P71364	GLUCONATE PERHEASE (GN 9.72e+01
35	40	78.4	562	9	P76923	SIMILAR TO. 9.72e+01
36	40	78.4	601	9	007176	HYPOHETICAL 68.6 KD P 9.72e+01
37	40	78.4	620	3	001909	SIMILARITY TO MULTIPLE 9.72e+01
38	40	78.4	635	3	018199	Y48B1B.5. 9.72e+01
39	40	78.4	659	3	018406	CODHD FOR BY C. ELEGAN 9.72e+01
40	40	78.4	747	3	020046	COSMID F35D2. 9.72e+01
41	40	78.4	801	2	015558	TESTIS DETERMINING FAC 9.72e+01
42	40	78.4	852	11	041593	ENVELOPE GLYCOPROTEIN 9.72e+01
43	40	78.4	861	11	071819	ENV GLYCOPROTEIN. 9.72e+01
44	40	78.4	862	11	073336	ENVELOPE POLYPROTEIN. 9.72e+01
45	40	78.4	1113	2	015056	KIA00348. 9.72e+01

ALIGNMENTS

RESULT 1
ID 063577 PRELIMINARY: PRT: 2505 AA.
AC 063577;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE FATTY ACID SYNTHASE
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89240686.
RA AMY C.M., WITKOWSKI A., NAGGERT J., WILLIAMS B., RANDHAVA Z.,
RA SMITH S.;
RL PROC. NATL. ACAD. SCI. U.S.A. 86:3114-3118(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92141210.
RA SMITH S., NAGGERT J., WILLIAMS-AHLF B., AMY C.M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 89:1105-1108(1992).
DR EMBL; M84761; G204099; .
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
KW TRANSFERASE
SO SEQUENCE 2505 AA; 272663 MW; 5151416A CRC32;
Query Match 88.2%; Score 45; DB 10; Length 2505;
Best Local Similarity 71.4%; Pred. No. 7.93e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 550 VHSFVSL 556
QY 1 VHNFFVAL 7
RESULT 2
ID 016702 PRELIMINARY: PRT: 2509 AA.
AC 016702;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE FATTY ACID SYNTHASE (EC 2.3.1.85) (FATTY-ACID SYNTHASE).
OS HOMO SAPIENS (HUMAN).

Thu Jul 30 13:38:07 1998

US-08-817-547A-25.rsp

Page 2

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA HENNIGAR R.A., JENNER K.H., HEINE H.S., KAYLER A.E., WOOD F.D.,
RA KOHAUDA F.P., PASTERNAK G.R.,
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH - A
CC LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+).
CC EMBL: U29344; G915392; -
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; 1.
DR PROSITE: PS00606; B. KETOACYL SYNTHASE; 1.
KM TRANSFERASE; ACYLTRANSFERASE
SQ SEQUENCE 2509 AA; 273089 MW; D1E74B76 CRC32;
Query Match 88.28; Score 45; DB 2; Length 2509;
Best Local Similarity 71.4%; Pred. No. 7.93e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
550 VHSFVSL 556
||:|:|:
1 VHNFEVAL 7

Search completed: Thu Jul 30 10:56:24 1998
Job time : 26 secs.

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:59:44 1998; MasPar time 2.58 Seconds
Tabular output not generated. 35.687 Million cell updates/sec

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 HNFVAL 6

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 1538987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.505; Variance 37.183; scale 0.390

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	44	100.0	38	9	R58142 [Asn21]-hPTH(1-38)-OH	4.86e+01
2	44	100.0	38	9	R58140 [Phe21]-hPTH(1-38)-OH	4.86e+01
3	44	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	4.86e+01
4	44	100.0	38	9	R58133 [Asp19]-hPTH(1-38)-OH	4.86e+01
5	44	100.0	44	26	P30015 Human parathyroid hor	4.86e+01
6	44	100.0	47	25	W21946 Fusion protein compri	4.86e+01
7	44	100.0	84	27	W25687 Human parathyroid hor	4.86e+01
8	44	100.0	84	4	R23134 Bovine parathyroid ho	4.86e+01
9	44	100.0	84	4	R23343 Bovine parathyroid ho	4.86e+01
10	44	100.0	84	4	R21199 Human parathyroid hor	4.86e+01
11	44	100.0	84	4	R23309 Bovine parathyroid h	4.86e+01
12	44	100.0	84	4	R23492 Porcine parathyroid h	4.86e+01
13	44	100.0	84	4	R23493 Porcine parathyroid h	4.86e+01
14	44	100.0	84	4	R23276 Bovine parathyroid ho	4.86e+01
15	44	100.0	84	4	R21254 Human parathyroid hor	4.86e+01
16	44	100.0	84	4	R23284 Porcine parathyroid h	4.86e+01
17	44	100.0	84	4	R23246 Human parathyroid hor	4.86e+01
18	44	100.0	84	4	R21175 Human parathyroid hor	4.86e+01
19	44	100.0	84	4	R21174 Human parathyroid hor	4.86e+01

20	44	100.0	84	4	R23424 Porcine parathyroid h	4.86e+01
21	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23383 Porcine parathyroid h</th> <th>4.86e+01</th>	100.0	84	4	R23383 Porcine parathyroid h	4.86e+01
22	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21161 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21161 Human parathyroid hor	4.86e+01
23	44 <th>100.0</th> <th>84</th> <th>5</th> <th>R29563 Oxidation resistant p</th> <th>4.86e+01</th>	100.0	84	5	R29563 Oxidation resistant p	4.86e+01
24	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21241 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21241 Human parathyroid hor	4.86e+01
25	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21240 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21240 Human parathyroid hor	4.86e+01
26	44 <th>100.0</th> <th>84</th> <th>25</th> <th>W29420 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	25	W29420 Human parathyroid hor	4.86e+01
27	44 <th>100.0</th> <th>84</th> <th>5</th> <th>R29562 Oxidation resistant p</th> <th>4.86e+01</th>	100.0	84	5	R29562 Oxidation resistant p	4.86e+01
28	44 <th>100.0</th> <th>84</th> <th>5</th> <th>R29561 Oxidation resistant p</th> <th>4.86e+01</th>	100.0	84	5	R29561 Oxidation resistant p	4.86e+01
29	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23248 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R23248 Human parathyroid hor	4.86e+01
30	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21250 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21250 Human parathyroid hor	4.86e+01
31	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21219 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21219 Human parathyroid hor	4.86e+01
32	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21187 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21187 Human parathyroid hor	4.86e+01
33	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23227 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R23227 Human parathyroid hor	4.86e+01
34	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21181 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21181 Human parathyroid hor	4.86e+01
35	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21234 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21234 Human parathyroid hor	4.86e+01
36	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21238 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21238 Human parathyroid hor	4.86e+01
37	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23392 Porcine parathyroid h</th> <th>4.86e+01</th>	100.0	84	4	R23392 Porcine parathyroid h	4.86e+01
38	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23433 Porcine parathyroid h</th> <th>4.86e+01</th>	100.0	84	4	R23433 Porcine parathyroid h	4.86e+01
39	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23374 Bovine parathyroid ho</th> <th>4.86e+01</th>	100.0	84	4	R23374 Bovine parathyroid ho	4.86e+01
40	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23240 Human parathyroid ho</th> <th>4.86e+01</th>	100.0	84	4	R23240 Human parathyroid ho	4.86e+01
41	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23456 Porcine parathyroid h</th> <th>4.86e+01</th>	100.0	84	4	R23456 Porcine parathyroid h	4.86e+01
42	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23363 Bovine parathyroid ho</th> <th>4.86e+01</th>	100.0	84	4	R23363 Bovine parathyroid ho	4.86e+01
43	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21210 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21210 Human parathyroid hor	4.86e+01
44	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R21211 Human parathyroid hor</th> <th>4.86e+01</th>	100.0	84	4	R21211 Human parathyroid hor	4.86e+01
45	44 <th>100.0</th> <th>84</th> <th>4</th> <th>R23449 Porcine parathyroid h</th> <th>4.86e+01</th>	100.0	84	4	R23449 Porcine parathyroid h	4.86e+01

ALIGNMENTS

RESULT 1
ID R58142 standard; peptide; 38 AA.
AC R58142;
DT 20-SEP-1994 (first entry)
DE [asn21]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (BAUER) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERM GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active parathyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 139; Page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;
Query Match 100.0%; Score 44; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.86e+01;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
Db 32 hnfval 37

OY 1 HNFVAL 6

RESULT 2
ID R58140 standard; peptide; 38 AA.

AC R58140;

DE [phe21]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.

OS Synthetic.

PN GB2269176-A.

PD 02-FEB-1994.

PE 12-JUL-1993; 014384.

PR 15-JUL-1992; GB-015009.

PR 18-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.

PR (SANO) SANDOZ LTD.

PA (BAVE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Palmer A;

PI WPI; 94-018352/03.

PT New active para-thyroid hormone variants - used for treating or

PT Preventing osteoporosis etc.

PS Example 137; Page 40; 92pp; English.

CC This peptide is an example of a highly generic formula covering

CC parathyroid hormone variants useful for treating or preventing bone

CC conditions associated with calcium depletion/resorption, in cases

CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

CC Sequence 38 AA;

SO

Query Match 100.0%; Score 44; DB 9; Length 38;

Best Local Similarity 100.0%; Pred. No. 4.86e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 hnfval 37

1 HNFVAL 6

Search completed: Thu Jul 30 10:59:59 1998

Job time : 15 secs.

WIDEVIEW (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:59:09 1998; Maspar time 3.02 Seconds
Tabular output not generated. 72.657 Million cell updates/sec

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 HNFVAL 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56

1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 20.121; Variance 22.615; scale 0.890

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	44	100.0	34	5 1ZWE	parathyroid hormone (6.34e+00	
2	44	100.0	34	5 1ZWE	parathyroid hormone (6.34e+00	
3	44	100.0	34	5 1ZWE	parathyroid hormone (6.34e+00	
4	44	100.0	35	5 1ZWD	parathyroid hormone (6.34e+00	
5	44	100.0	36	5 1ZWB	parathyroid hormone (6.34e+00	
6	44	100.0	37	5 1ZWB	parathyroid hormone (6.34e+00	
7	44	100.0	37	5 1ZWB	parathyroid hormone (6.34e+00	
8	44	100.0	37	5 1ZWB	parathyroid hormone (6.34e+00	
9	44	100.0	115	1 PTHU	parathyroid hormone P 6.34e+00	
10	44	100.0	115	1 PTHU	parathyroid hormone P 6.34e+00	
11	44	100.0	115	1 PTHU	parathyroid hormone P 6.34e+00	
12	42	95.5	105	2 151851	parathyroid hormone P 1.77e+01	
13	42	95.5	115	2 A05091	parathyroid hormone P 1.77e+01	
14	42	95.5	541	2 A25696	yellow protein - fru1 4.76e+01	
15	40	90.9	429	2 F64966	hypothetical protein 4.76e+01	
16	40	90.9	408	2 A37813	UDP-N-acetylglucosam 4.76e+01	
17	40	90.9	410	2 S24326	UDP-N-acetylglucosam 4.76e+01	
18	40	90.9	430	2 JQ1184	osteogenic protein 1 4.76e+01	
19	40	90.9	431	1 BMH07	bone morphogenetic pr 4.76e+01	
20	40	90.9	507	2 A39939	protein-tyrosine kina 4.76e+01	
21	40	90.9	578	2 D64933	yfaa protein - Escher 4.76e+01	
22	40	90.9	581	2 G70189	threonine--trna ligas 4.76e+01	
23	40	90.9	924	2 S34926	hypothetical protein 4.76e+01	

24	40	90.9	997	2 A60776	230k bullous pemphig 4.76e+01
25	39	88.6	136	2 S73520	Mg441 homolog E09.orf 7.71e+01
26	39	88.6	201	2 C65188	hypothetical 22.3 kd 7.71e+01
27	39	88.6	208	2 J05638	pH-sensing regulatory 7.71e+01
28	39	88.6	212	2 S39965	hypothetical protein 7.71e+01
29	39	88.6	227	2 S39965	ubiquitin thiolstera 7.71e+01
30	39	88.6	259	2 D69598	maturatin of the cut 7.71e+01
31	39	88.6	504	2 140811	uroporphyrinogen-III 7.71e+01
32	39	88.6	707	2 S43297	oligopeptide transpor 7.71e+01
33	39	88.6	708	2 A56163	peptide transport pro 7.71e+01
34	39	88.6	710	2 S68161	oligopeptide transpor 7.71e+01
35	39	88.6	710	2 S72497	oligopeptide transpor 7.71e+01
36	39	88.6	798	2 JN0878	100k protein - fowl a 7.71e+01
37	39	88.6	885	2 S67660	hypothetical protein 7.71e+01
38	38	86.4	388	2 S04110	integrinase - streptom 1.24e+02
39	38	86.4	397	2 G69287	hypothetical protein 1.24e+02
40	38	86.4	409	2 A42363	peptidase T - Salmons 1.24e+02
41	38	86.4	508	2 G69593	endo-1,4-beta-glucana 1.24e+02
42	38	86.4	582	2 A49626	transregulatory prote 1.24e+02
43	38	86.4	604	2 S66993	hypothetical protein 1.24e+02
44	38	86.4	711	2 E69121	conserved hypotherica 1.24e+02
45	38	86.4	2504	2 A57788	fatty-acid synthase (1.24e+02

ALIGNMENTS

RESULT	1	1ZWE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:1ZWE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
COMMENT		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
KEYWORDS		Resolution: not applicable	
FEATURE		Determination: NMR	
15-25		hormone	
SUMMARY		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 44; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 6.34e+00;	
Matches		6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	29	HNFVAL 34	
Qy	1	HNFVAL 6	
RESULT	2	1ZWE	#type complete
ENTRY		parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:1ZWE	
REFERENCE		TN003319	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 2-9 #region helix (right hand alpha)\
 15-25 #region helix (right hand alpha)
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 44; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.34e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 HNFVAL 34
 |||||
 QY 1 HNFVAL 6

Search completed: Thu Jul 30 10:59:26 1998
 Job time : 17 secs.

M O S E R
(TM)

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Msearch.p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:57:48 1998; Maspar time 2.03 Seconds
74.131 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 HNFVAL 6

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 21.045; Variance 18.682; scale 1.127

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	44	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.12e+00
2	44	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.12e+00
3	44	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	1.12e+00
4	44	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.12e+00
5	42	95.5	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.84e+00
6	42	95.5	115	1	PTHY_MOUSE PARATHYROID HORMONE PR	3.84e+00
7	40	90.9	408	1	YELL_DROME YELLOW PROTEIN.	1.26e+01
8	40	90.9	408	1	GPT_CRIGR UDP-N-ACETYLGLUCOSAMIN	1.26e+01
9	40	90.9	430	1	GPT_MOUSE UDP-N-ACETYLGLUCOSAMIN	1.26e+01
10	40	90.9	430	1	BMP7_MOUSE BONE MORPHOGENETIC PRO	1.26e+01
11	40	90.9	431	1	BMP7_HUMAN BONE MORPHOGENETIC PRO	1.26e+01
12	40	90.9	507	1	LCK_CHICK PROTO-ONCOGENE TYROSIN	1.26e+01
13	40	90.9	578	1	YFSA_YEAST HYPOTHETICAL 64.5 KD P	1.26e+01
14	40	90.9	924	1	YFSA_YEAST HYPOTHETICAL 104.5 KD P	1.26e+01
15	39	88.6	104	1	CGEE_BACSU CGEE PROTEIN (FRAGMENT	2.23e+01
16	39	88.6	136	1	Y441_MYCPN HYPOTHETICAL PROTEIN M	2.23e+01
17	39	88.6	200	1	YICP_ECOLI HYPOTHETICAL 22.3 KD P	2.23e+01
18	39	88.6	227	1	UBI_DROME UBIQUITIN CARBOXYL-TER	2.23e+01
19	39	88.6	504	1	HEW4_CLOUD UROPOPHYRIN-III C-MET	2.23e+01
20	39	88.6	707	1	HEW4_CLOUD UROPOPHYRIN-III C-MET	2.23e+01
21	39	88.6	708	1	PEP1_RABIT OLIGOPEPTIDE TRANSPORT	2.23e+01
22	39	88.6	710	1	PEP1_RAT OLIGOPEPTIDE TRANSPORT	2.23e+01
23	39	88.6	798	1	L100_ADEGX LATE 100 KD PROTEIN.	2.23e+01

24	39	88.6	984	1	L100_ADEGX LATE 100 KD PROTEIN.	2.23e+01
25	38	86.4	249	1	UL07_HSV6U PROTEIN U75.	3.91e+01
26	38	86.4	249	1	UL07_HSV6Z PROTEIN U75.	3.91e+01
27	38	86.4	259	1	UDP_HAELN URIDINE PHOSPHORYLASE	3.91e+01
28	38	86.4	289	1	ROB_ECOLI RIGHT ORIGIN-BINDING P	3.91e+01
29	38	86.4	297	1	YMW9_YEAST HYPOTHETICAL 34.0 KD P	3.91e+01
30	38	86.4	388	1	INTR_STRAM INTRIGASE.	3.91e+01
31	38	86.4	408	1	PEPT_ECOLI PEPTIDASE T (EC 3.4.11	3.91e+01
32	38	86.4	409	1	PEPT_SALTY PEPTIDASE T (EC 3.4.11	3.91e+01
33	38	86.4	499	1	GUN2_BACSU ENDOGLUCANASE PRECURSO	3.91e+01
34	38	86.4	499	1	GUN1_BACSU ENDOGLUCANASE PRECURSO	3.91e+01
35	38	86.4	536	1	YB36_YEAST HYPOTHETICAL 60.5 KD P	3.91e+01
36	38	86.4	541	1	DETI_ARATH LIGHT-MEDIATED DEVELOP	3.91e+01
37	38	86.4	560	1	TATR_NPVCE TRANS-ACTIVATING TRANS	3.91e+01
38	38	86.4	560	1	TATR_NPVOP TRANS-ACTIVATING TRANS	3.91e+01
39	38	86.4	582	1	TATR_NPVAC TRANS-ACTIVATING TRANS	3.91e+01
40	38	86.4	587	1	TATR_NPVAM TRANS-ACTIVATING TRANS	3.91e+01
41	38	86.4	591	1	LACI_CRYPA LACCASE PRECURSOR (EC	3.91e+01
42	38	86.4	687	1	CSTA_HELPY CARBON STARVATION PROT	3.91e+01
43	38	86.4	790	1	TNP3_HUMAN TUMOR NECROSIS FACTOR,	3.91e+01
44	38	86.4	2504	1	FAS_HUMAN FATTY ACID SYNTHASE (E	3.91e+01
45	38	86.4	2505	1	FAS_RAT FATTY ACID SYNTHASE (E	3.91e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	115 AA.
ID	PTHY_CANFA			
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
NC	EUTHERIA; CARNIVORA.			
RC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PARATHYROID;			
RX	MEDLINE: 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RL	DEVILLE J.W., CAPEN C.C.;			
RL	GENE 160:241-243(1995).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL: U15662; G558916; -.			
DR	PROSITE: PS00335; PARATHYROID: 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL			
FT	PROPEP			
FT	CHAIN			
SO	SEQUENCE			
Query Match	100.0%;	Score 44;	DB 1;	Length 115;
Best Local Similarity	100.0%;	Pred. No. 1.12e+00;		
Matches	6;	Conservative	0;	Mismatches 0;
Indels			0;	Gaps 0;
Db	63 HNFVAL 68			
Qy	1 HNFVAL 6			
RESULT	2	STANDARD;	PRT;	115 AA.
ID	PTHY_BOVIN			
AC	P01268;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	BOS Taurus (BOVINE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

Search completed: Thu Jul 30 10:57:54 1998
Job time : 6 secs.

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZUB J.A., NATHANS J., SHARP P.A.,
RN [2]
PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAYER C.A., GORDON D.F., KEMPER B.,
RN [3]
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAYER C.A., GORDON D.F., KEMPER B.,
RN [4]
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAYER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.,
RN [5]
GENE 28:319-329(1984).
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RN [6]
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RN [7]
AURBACH G.D., POTTS J.T. JR.,
HOPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREMER H.B. JR., RONAN R.,
RN [8]
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RN [9]
DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.,
PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: V00106; 685; -.
EMBL: J00023; G163641; -.
EMBL: J00024; G163643; -.
EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01938; G163647; -.
EMBL: M25082; G163645; -.
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
KM HORMONE; SIGNAL.
FT SIGNAL. 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EASF2 CRC32;

Query Match 100.0%; Score 44; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.12e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 63 HNFVAL 68
OY 1 HNFVAL 6

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(TW)

Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:58:11 1998; MasPar time 3.65 Seconds
69.158 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 HNFVAL 6

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 20.282; Variance 20.253; scale 1.001

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	42	95.5	105	10	063473	PARATHYROID HORMONE (F	1.01e+01
2	42	95.5	568	3	002437	YELLOW	1.01e+01
3	42	95.5	2408	2	092566	MELOBLAST KIAA0279 (F	1.01e+01
4	41	93.2	1149	3	023315	ZC434.5.	1.76e+01
5	41	93.2	1774	3	093636	F2966.3B.	1.76e+01
6	41	93.2	1918	3	093637	F2966.3A.	1.76e+01
7	40	90.9	296	9	P76472	FROM BASES 2360084 TO	3.04e+01
8	40	90.9	400	2	015216	GLCNAC-1-P TRANSFERASE	3.04e+01
9	40	90.9	562	9	P76923	SIMILAR TO.	3.04e+01
10	40	90.9	635	3	018199	Y48E1B.5.	3.04e+01
11	40	90.9	747	3	020046	COSMID F35D2.	3.04e+01
12	39	88.6	154	3	016894	BAHAMA HEMOLYMPH POLYP	5.18e+01
13	39	88.6	208	2	014496	PH-SENSING REGULATOR	5.18e+01
14	39	88.6	208	9	033707	PUTATIVE EXIMERASE.	5.18e+01
15	39	88.6	212	9	054198	DNA SEQUENCE FOR ORF'S	5.18e+01
16	39	88.6	554	3	009995	PUTATIVE POLY(A) POLYM	5.18e+01
17	39	88.6	635	1	013781	HYPOTHETICAL 71.4 KD P	5.18e+01
18	39	88.6	726	9	032971	ABC-TYPE TRANSPORTER.	5.18e+01
19	39	88.6	805	3	013305	SIMILAR TO F-SPONIN.	5.18e+01
20	39	88.6	885	1	007533	CHROMOSOME IV READING	5.18e+01

ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
21	38	86.4	119	11	083954	OCCULTION DERIVED	8.72e+01
22	38	86.4	232	3	020262	CODED FOR BY C. ELEGAN	8.72e+01
23	38	86.4	380	9	028847	PHOSPHONOPYRUVATE DECA	8.72e+01
24	38	86.4	397	9	029939	HYPOTHETICAL 46.5 KD P	8.72e+01
25	38	86.4	499	9	045532	CELLULOSE.	8.72e+01
26	38	86.4	562	9	058311	HYPOTHETICAL PROTEIN M	8.72e+01
27	38	86.4	582	11	086702	IE-1.	8.72e+01
28	38	86.4	604	6	035126	CYCLOHOME C OXIDASE S	8.72e+01
29	38	86.4	604	1	021166	YOR3227W FROM CHROMOSO	8.72e+01
30	38	86.4	711	9	027928	OLIGOSACCHARYL TRANSFE	8.72e+01
31	38	86.4	1226	1	006836	SIMILARITY TO T1PA.	8.72e+01
32	38	86.4	1634	2	000750	PHOSPHONOSITIDE 3-KIN	8.72e+01
33	38	86.4	2505	2	063577	FATTY ACID SYNTHASE.	8.72e+01
34	38	86.4	2509	2	026702	WHITE (FRAGMENT).	8.72e+01
35	37	84.1	243	3	002409	PYRIDINE NUCLEOTIDE TR	1.45e+02
36	37	84.1	480	9	P73500	MC1311.	1.45e+02
37	37	84.1	513	11	098297	EQUINE ARTERITIS VIRUS	1.45e+02
38	37	84.1	540	11	083024	ENVIOLE GLYCOPROTEIN.	1.45e+02
39	37	84.1	885	11	069387	GB GLYCOPROTEIN.	1.45e+02
40	37	84.1	891	11	066018	GLYCOPROTEIN B PRECURS	1.45e+02
41	37	84.1	902	11	069095	GLYCOPROTEIN B PRECURS	1.45e+02
42	37	84.1	904	11	037453	PYRIDINE NUCLEOTIDE TRA	1.45e+02
43	37	84.1	1083	3	024858	POLYPROTEIN 1B (FRAGME	1.45e+02
44	37	84.1	1410	11	083018	POL POLYPROTEIN (CONTA	1.45e+02
45	37	84.1	1411	11	006503		

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	95.5%	105	10	063473	PARATHYROID HORMONE (F	1.01e+01	
2	063473	95.5%	568	3	002437	YELLOW	1.01e+01	
3	063473	95.5%	2408	2	092566	MELOBLAST KIAA0279 (F	1.01e+01	
4	063473	95.5%	1149	3	023315	ZC434.5.	1.76e+01	
5	063473	95.5%	1774	3	093636	F2966.3B.	1.76e+01	
6	063473	95.5%	1918	3	093637	F2966.3A.	1.76e+01	
7	063473	95.5%	296	9	P76472	FROM BASES 2360084 TO	3.04e+01	
8	063473	95.5%	400	2	015216	GLCNAC-1-P TRANSFERASE	3.04e+01	
9	063473	95.5%	562	9	P76923	SIMILAR TO.	3.04e+01	
10	063473	95.5%	635	3	018199	Y48E1B.5.	3.04e+01	
11	063473	95.5%	747	3	020046	COSMID F35D2.	3.04e+01	
12	063473	95.5%	154	3	016894	BAHAMA HEMOLYMPH POLYP	5.18e+01	
13	063473	95.5%	208	2	014496	PH-SENSING REGULATOR	5.18e+01	
14	063473	95.5%	208	9	033707	PUTATIVE EXIMERASE.	5.18e+01	
15	063473	95.5%	212	9	054198	DNA SEQUENCE FOR ORF'S	5.18e+01	
16	063473	95.5%	554	3	009995	PUTATIVE POLY(A) POLYM	5.18e+01	
17	063473	95.5%	635	1	013781	HYPOTHETICAL 71.4 KD P	5.18e+01	
18	063473	95.5%	726	9	032971	ABC-TYPE TRANSPORTER.	5.18e+01	
19	063473	95.5%	805	3	013305	SIMILAR TO F-SPONIN.	5.18e+01	
20	063473	95.5%	885	1	007533	CHROMOSOME IV READING	5.18e+01	

RP SEQUENCE FROM N.A.
 RA SAGARRA C.; TO EMBL/GENBANK/DBJ DATA BANKS.
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; Y13909; E324295; -
 DR FLXBASE; FB9N0015179; DsubV.
 SQ SEQUENCE 568 AA; 62589 MW; 6F52A641 CRC32;

Query Match 95.5%; Score 42; DB 3; Length 568;
 Best Local Similarity 83.3%; Pred. No. 1.01e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 301 HDEFVAL 306
 Oy 1 HDEFVAL 6

Search completed: Thu Jul 30 10:58:51 1998
 Job time : 40 secs.

MIPARCH
(TM)

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MIPARCH protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:02:08 1998; MasPar time 2.54 Seconds
30.164 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-27
Description: (1-5) from US08817547A.pep
Perfect Score: 35
Sequence: 1 NEFVAL 5

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.768; Variance 32.782; scale 0.420

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	35	100.0	38	9	R58019 N-alpha-methyl[Ala1]	3.36e+02
2	35	100.0	38	9	R58126 [Ala19]-hPTH(1-38)-OH	3.36e+02
3	35	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	3.36e+02
4	35	100.0	38	9	R58133 [Asp19]-hPTH(1-38)-OH	3.36e+02
5	35	100.0	44	26	P30015 Human parathyroid hor	3.36e+02
6	35	100.0	47	25	W21945 Fusion protein compri	3.36e+02
7	35	100.0	84	27	W25687 Human parathyroid hor	3.36e+02
8	35	100.0	84	4	R23524 Human parathyroid hor	3.36e+02
9	35	100.0	84	4	R23227 Human parathyroid hor	3.36e+02
10	35	100.0	84	4	R21199 Human parathyroid hor	3.36e+02
11	35	100.0	84	4	R23309 Bovine parathyroid ho	3.36e+02
12	35	100.0	84	4	R23396 Porcine parathyroid h	3.36e+02
13	35	100.0	84	4	R23435 Porcine parathyroid h	3.36e+02
14	35	100.0	84	4	R21255 Human parathyroid hor	3.36e+02
15	35	100.0	84	4	R21254 Human parathyroid hor	3.36e+02
16	35	100.0	84	4	R21179 Human parathyroid hor	3.36e+02
17	35	100.0	84	4	R23332 Bovine parathyroid hor	3.36e+02
18	35	100.0	84	4	R23501 Porcine parathyroid h	3.36e+02
19	35	100.0	84	4	R23500 Porcine parathyroid h	3.36e+02

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	R58019	35	100.0	38	4	R21161 Human parathyroid hor	3.36e+02
2	AC	35	100.0	84	4	R21160 Human parathyroid hor	3.36e+02
3	DT	35	100.0	84	25	W29420 Human parathyroid hor	3.36e+02
4	DE	35	100.0	84	5	R29562 Oxidation resistant l	3.36e+02
5	KW	35	100.0	84	4	R29561 Oxidation resistant p	3.36e+02
6	KW	35	100.0	84	4	R23478 Porcine parathyroid h	3.36e+02
7	KW	35	100.0	84	4	R23346 Bovine parathyroid ho	3.36e+02
8	KW	35	100.0	84	4	R21219 Human parathyroid hor	3.36e+02
9	KW	35	100.0	84	4	R23353 Bovine parathyroid hor	3.36e+02
10	KW	35	100.0	84	4	R23379 Bovine parathyroid ho	3.36e+02
11	KW	35	100.0	84	4	R23260 Bovine parathyroid ho	3.36e+02
12	KW	35	100.0	84	4	R23336 Bovine parathyroid ho	3.36e+02
13	KW	35	100.0	84	4	R23392 Porcine parathyroid h	3.36e+02
14	KW	35	100.0	84	4	R23433 Porcine parathyroid h	3.36e+02
15	KW	35	100.0	84	4	R23384 Porcine parathyroid h	3.36e+02
16	KW	35	100.0	84	4	R23246 Human parathyroid hor	3.36e+02
17	KW	35	100.0	84	4	R21175 Human parathyroid hor	3.36e+02
18	KW	35	100.0	84	4	R21174 Human parathyroid hor	3.36e+02
19	KW	35	100.0	84	4	R21210 Human parathyroid hor	3.36e+02
20	KW	35	100.0	84	4	R21211 Human parathyroid hor	3.36e+02
21	KW	35	100.0	84	5	R29563 Oxidation resistant P	3.36e+02
22	KW	35	100.0	115	13	R75693 Human prepro-PTH	3.36e+02
23	KW	35	100.0	115	25	W23060 Mouse beta 2 integrin	3.36e+02
24	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
25	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
26	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
27	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
28	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
29	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
30	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
31	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
32	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
33	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
34	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
35	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
36	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
37	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
38	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
39	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
40	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
41	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
42	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
43	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
44	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
45	KW	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02

ALIGNMENTS

RESULT 1
ID R58019 standard; peptide: 38 AA.
AC R58019; 20-SEP-1994 (first entry)
DE N-alpha-methyl[Ala1] parathyroid hormone(1-38).
KW Human parathyroid hormone; hPTH; variant; analogue;
KW Calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 1 /note="N-alpha-methyl-Ala replaces wild-type
Ser residue at position 1"
FT Ser residue at position 1"
FN
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUER) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R. Bauer W. Breckenridge R. Cardinaux F.
PI Gombert F. Gram H. Lewis I. Ramage P. Schneider H.
PI Maechli R. Rainer A.
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 4; Page 34; 92pp; English.
CC This peptide is an highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption. In cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 35; DB 9; Length 38;

Best Local Similarity 100.0%; Pred. No. 3.36e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 33 nival 37
| | | | |
QY 1 NIVAL 5

RESULT 2
ID R58126 standard; peptide; 38 AA.
AC R58126;
DT 20-SEP-1994 (first entry)
DE [Ala19]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PT 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Maelchli R, Rainer A.
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 123; Page 39; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 35; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.36e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
33 nival 37
| | | | |
QY 1 NIVAL 5

Search completed: Thu Jul 30 11:02:23 1998
Job time : 15 secs.

WIDEVIEW (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:01:26 1998; MasPar time 3.08 Seconds
59.234 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-27
Description: (1-5) from US08817547A.pep
Perfect Score: 35
Sequence: 1 NFWAL 5

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 19.157; Variance 19.754; scale 0.970

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	35	100.0	34	5	1ZWF parathyroid hormone 4	1.85e+02
2	35	100.0	34	5	1ZMG parathyroid hormone 4	1.85e+02
3	35	100.0	34	5	1ZWE parathyroid hormone 4	1.85e+02
4	35	100.0	35	5	1ZMB parathyroid hormone 4	1.85e+02
5	35	100.0	36	5	1ZWB parathyroid hormone 4	1.85e+02
6	35	100.0	37	5	1ZWC parathyroid hormone 4	1.85e+02
7	35	100.0	37	5	1ZWP parathyroid hormone 4	1.85e+02
8	35	100.0	46	2	S45724 parathyroid hormone 4	1.85e+02
9	35	100.0	87	2	S21218 parathyroid hormone 4	1.85e+02
10	35	100.0	115	1	PTBO parathyroid hormone 4	1.85e+02
11	35	100.0	115	2	JC4202 parathyroid hormone 4	1.85e+02
12	35	100.0	115	1	PTHU parathyroid hormone 4	1.85e+02
13	35	100.0	115	1	PTHU parathyroid hormone 4	1.85e+02
14	35	100.0	140	2	A69445 parathyroid hormone 4	1.85e+02
15	35	100.0	178	5	1CYNA cyclophilin b, chain	1.85e+02
16	35	100.0	182	5	2RMCE cyclophilin c complex	1.85e+02
17	35	100.0	182	5	2RMCG cyclophilin c complex	1.85e+02
18	35	100.0	182	5	2RMCC cyclophilin c complex	1.85e+02
19	35	100.0	182	5	2RMCA cyclophilin c complex	1.85e+02
20	35	100.0	183	2	S71547 peptidylprolyl isomer	1.85e+02
21	35	100.0	201	2	C65188 hypothetical 22.3 kd	1.85e+02
22	35	100.0	207	2	A40516 peptidylprolyl isomer	1.85e+02
23	35	100.0	208	1	CSHUB peptidylprolyl isomer	1.85e+02

24	35	100.0	212	2	A40047	peptidylprolyl isomer	1.85e+02
25	35	100.0	212	2	A54204	peptidylprolyl isomer	1.85e+02
26	35	100.0	215	2	S75497	hypothetical protein	1.85e+02
27	35	100.0	216	2	A56861	peptidylprolyl isomer	1.85e+02
28	35	100.0	292	2	G69417	conserved hypothetical	1.85e+02
29	35	100.0	345	2	S73498	MG456 homolog K05orf	1.85e+02
30	35	100.0	352	2	JT0321	photosystem II protei	1.85e+02
31	35	100.0	362	2	JQ1602	replication protein B	1.85e+02
32	35	100.0	448	1	B26981	C4-dicarboxylate tran	1.85e+02
33	35	100.0	460	1	C33586	ADP-heptose synthase	1.85e+02
34	35	100.0	476	2	C64127	hypothetical protein	1.85e+02
35	35	100.0	533	2	S74401	probable membrane pro	1.85e+02
36	35	100.0	538	2	S64842	equine artemisin vitu	1.85e+02
37	35	100.0	540	2	B40901	aard protein - Provid	1.85e+02
38	35	100.0	588	2	S70900	mdlb protein - Escher	1.85e+02
39	35	100.0	593	2	A64775	SE66 protein - yeast	1.85e+02
40	35	100.0	805	2	S48411	hypothetical protein	1.85e+02
41	35	100.0	879	2	S73757	hypothetical protein	1.85e+02
42	35	100.0	1139	2	S28277	mdl protein - Escheri	1.85e+02
43	35	100.0	1143	2	I84547	transcription factor	1.85e+02
44	35	100.0	1160	2	A46423	protein disulfide iso	4.83e+02
45	33	94.3	517	2	A44483		

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE 1ZWF #type complete
parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -
synthetic
ALTERNATE_NAMES
PDB_TITLE n-acetyl-hpnh(4-37)
structure of n-terminal acetylated human parathyroid hormone,
NMR, 10 structures
ORGANISM #formal_name synthetic
REFERENCE A67742
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:1ZWF
REFERENCE TN003318
#authors Marx, U.C.
#book in Strukturen Verschiedener Parathormonfragmente in Loessung,
pp.0, Bayreuth: University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
KEYWORDS Determination: NMR
FEATURE
3-6 disease mutation; hormone; signal
14-27 #region helix (right hand alpha)\
SUMMARY #region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 35; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.85e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 30 NFWAL 34
QY 1 NFWAL 5

RESULT 2
ENTRY 1ZMG #type complete
parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -
synthetic
ALTERNATE_NAMES
PDB_TITLE n-succinyl-n-phth(4-37)
succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM #formal_name synthetic
REFERENCE A67743
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:1ZMG
REFERENCE TN003319
#authors Marx, U.C.
#book in Strukturen Verschiedener Parathormonfragmente in Loessung,

COMMENT pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
 RESOLUTION: not applicable
 DETERMINATION: NMR
 KEYWORDS
 FEATURE
 2-9
 15-25
 SUMMARY
 #region helix (right hand alpha) \
 #region helix (right hand alpha) \
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 35; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.85e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 30 NRYAL 34
 QY 1 NRYAL 5

Search completed: Thu Jul 30 11:01:50 1998
 Db time : 24 secs.

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIOURDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059320.
 RA TREGEAR G.W., VAN RIENSCHOTEN J., GREEN E., NIALL H.D.,
 KEUTMANN H.T., PARSONS J.A., O'RIOURDAN J.L.H., POTTS J.T. JR.;
 RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA RINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93453518.
 RA BARDEN J.A., CUTHERSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MARX U.C., AUSTERMANN S., BAYER P., ADERHANN K., EUSCHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FHH).
 DR EMBL: J00301; G190704; -.
 DR EMBL: V00597; G37144; -.
 DR EMBL: A29146; E186700; -.
 DR PIR: A01536; PTHU
 DR PIR: A19339; A19338.
 DR PDB: 1HPH; 10-JUL-95.
 DR PDB: 1HTH; 15-OCT-97.
 DR PDB: 1ZMA; 12-MAR-97.
 DR PDB: 1ZMB; 12-MAR-97.
 DR PDB: 1ZWC; 12-MAR-97.
 DR PDB: 1ZWD; 12-MAR-97.
 DR PDB: 1ZWE; 12-MAR-97.
 DR PDB: 1ZWF; 16-JUN-97.
 DR PDB: 1ZWG; 16-JUN-97.
 DR MIM: 146200; -.
 DR MIM: 168450; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 KM SIGNAL; 1
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA; 12861 MM; 243E87C7 CRC32;
 SQ
 Query Match 100.0%; Score 35; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6.41e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 64 NEVAL 68
 11111
 QY 1 NEVAL 5
 RESULT 2
 ID PTHY_BOVIN STANDARD; PRT; 115 AA.
 AC P01268;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 80056617.
 RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
 RA POTTS J.T. JR., RICH A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 82037785.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 83105964.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84262483.
 RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
 RL GENE 28:319-329(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 74142666.
 RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
 RA COHN D.V.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
 RN [6]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 71076162.
 RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
 RA AUBRACH G.D., POTTS J.T. JR.;
 RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
 RN [7]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 71063634.
 RA BREMER H.B. JR., RONAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 71091588.
 RA POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
 RA DEFTOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971)
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL: V00106; G85; -.
 DR EMBL: J00023; G163641; -.
 DR EMBL: J00024; G163643; -.
 DR EMBL: J00024; E18249; ALT_SEQ.
 DR EMBL: J00024; E18250; ALT_INIT.
 DR EMBL: K01938; G163647; -.
 DR EMBL: M25082; G163645; -.
 DR PIR: A01534; PTHO.
 DR PIR: A24949; A24949.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR HORMONE; SIGNAL.
 KM

FT SIGNAL 1 25
 FT PROPER 26 31
 FT CHAIN 32 115
 FT CONFLICT 106 106
 SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;
 PARATHYROID HORMONE.
 V -> G (IN REF. 4).

Query Match 100.0%; Score 35; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6.41e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64 NVAL 68
 QY 1 NVAL 5

Search completed: Thu Jul 30 11:00:22 1998
 Job time : 7 secs.

Db 87 NFEVAL 91
OY 1 NFEVAL 5

RESULT 2
ID P73988 PRELIMINARY; PRT; 215 AA.
AC P73988;

DT 01-FEB-1997 (TREMBLREL. 02, CREATED)

DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 23.8 KD PROTEIN.

OS SYNECHOCYSTIS SP.

OC EUBACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-PCC6803;

RA TABATA S.;

RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DOBJ DATA BANKS.

RA [2]
SEQUENCE FROM N.A.

RA STRAIN-PCC6803;

RA KANERO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,

RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,

RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARDO K.,

RA OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A.,

RA YAMADA M., YASUDA M., TABATA S.;

RL DNA RES. 3:109-136(1996).

DR EMBL; D90911; G1653142; -.

KW HYPOTHETICAL PROTEIN.







SO SEQUENCE 215 AA; 23768 MW; 329FA3F6 CRC32;

Query Match 100.0%; Score 35; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.56e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 128 NFEVAL 132
OY 1 NFEVAL 5

Search completed: Thu Jul 30 11:01:07 1998
Job time : 26 secs.

Query Match 100.0%; Score 95; DB 9; Length 36;
 Best Local Similarity 100.0%; Pred. No. 6.12e-03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 lrrklqdvhnfv 36
 |||||
 QY 1 LRRKLQDVHNFEVA 13

RESULT 2

ID R58052 standard; peptide; 36 AA.

AC R58052:

DE [LE,Al7,Q18,Al9]-hPTH(1-36)-OH.

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

OS Synthetic.

GB2269176-A.

02-FEB-1994.

12-JUL-1993.

PR 15-JUL-1992; GB-015009.

PR 18-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026861.

PR 28-JAN-1993; GB-001691.

PR 28-JAN-1993; GB-001692.

PR 14-APR-1993; GB-007673.

PR 19-APR-1993; GB-008033.

PA (SANO) SANDOZ LTD.

PA (BAUER) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PI (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

DR WPI; 94-018352/03.

PT New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

PS Example 45; Page 36; 92pp; English.

CC This peptide is an example of a highly generic formula covering

CC parathyroid hormone variants useful for treating or preventing bone

CC conditions associated with calcium depletion/resorption, in cases

CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

SQ Sequence 36 AA;

Query Match 100.0%; Score 95; DB 9; Length 36;

Best Local Similarity 100.0%; Pred. No. 6.12e-03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 lrrklqdvhnfv 36
 |||||
 QY 1 LRRKLQDVHNFEVA 13

Search completed: Thu Jul 30 11:04:57 1998
 Job time : 22 secs.

WIREIMAGE (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:03:49 1998; MasPar time 3.36 Seconds
Tabular output not generated. 141.457 Million cell updates/sec

Title: >US-08-817-547A-28
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 LRKKLDVHNFEVA 13

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 26.057; Variance 41.730; scale 0.624

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	95	100.0	34	5 12WE	parathyroid hormone (1.21e-06	
2	95	100.0	34	5 12WE	parathyroid hormone (1.21e-06	
3	95	100.0	34	5 12WE	parathyroid hormone (1.21e-06	
4	95	100.0	35	5 12WB	parathyroid hormone (1.21e-06	
5	95	100.0	36	5 12WB	parathyroid hormone (1.21e-06	
6	95	100.0	37	5 12WB	parathyroid hormone (1.21e-06	
7	95	100.0	37	5 12WB	parathyroid hormone (1.21e-06	
8	95	100.0	115	1 PTHU	parathyroid hormone (1.21e-06	
9	95	100.0	115	1 JCA4202	parathyroid hormone (1.21e-06	
10	95	100.0	115	1 PTHG	parathyroid hormone (1.21e-06	
11	95	100.0	115	1 PTHG	parathyroid hormone (1.21e-06	
12	93	97.9	115	1 PTHG	parathyroid hormone (1.21e-06	
13	84	88.4	34	5 12WA	parathyroid hormone (1.86e-04	
14	84	88.4	34	5 12WA	parathyroid hormone (1.86e-04	
15	83	87.4	105	2 S15851	parathyroid hormone (2.90e-04	
16	66	69.5	2475	2 S15307	parathyroid hormone (3.96e-01	
17	64	67.4	444	2 S09681	citrate transport pro 8.77e-01	
18	58	61.1	183	2 S42547	glucose-1-phosphate a 8.76e+00	
19	58	61.1	330	2 S15145	myc protein - African 8.76e+00	
20	58	61.1	419	1 TVXLWC	transforming protein 8.76e+00	
21	57	60.0	281	2 S41854	phosphoprotein phosph 1.27e+01	
22	57	60.0	525	2 C64313	hypothetical protein 1.27e+01	
23	56	58.9	208	2 S20583	DNA-directed RNA poly 1.83e+01	

24	56	58.9	445	2	S43492	surface antigen - hep 1.83e+01
25 <td>55<td>57.9<td>102<td>2<td>S53076<td>probable membrane pro 2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>102<td>2<td>S53076<td>probable membrane pro 2.63e+01</td></td></td></td></td>	57.9 <td>102<td>2<td>S53076<td>probable membrane pro 2.63e+01</td></td></td></td>	102 <td>2<td>S53076<td>probable membrane pro 2.63e+01</td></td></td>	2 <td>S53076<td>probable membrane pro 2.63e+01</td></td>	S53076 <td>probable membrane pro 2.63e+01</td>	probable membrane pro 2.63e+01
26 <td>55<td>57.9<td>119<td>2<td>A34937<td>parathyroid hormone p 2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>119<td>2<td>A34937<td>parathyroid hormone p 2.63e+01</td></td></td></td></td>	57.9 <td>119<td>2<td>A34937<td>parathyroid hormone p 2.63e+01</td></td></td></td>	119 <td>2<td>A34937<td>parathyroid hormone p 2.63e+01</td></td></td>	2 <td>A34937<td>parathyroid hormone p 2.63e+01</td></td>	A34937 <td>parathyroid hormone p 2.63e+01</td>	parathyroid hormone p 2.63e+01
27 <td>55<td>57.9<td>203<td>2<td>S20584<td>DNA-directed RNA poly 2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>203<td>2<td>S20584<td>DNA-directed RNA poly 2.63e+01</td></td></td></td></td>	57.9 <td>203<td>2<td>S20584<td>DNA-directed RNA poly 2.63e+01</td></td></td></td>	203 <td>2<td>S20584<td>DNA-directed RNA poly 2.63e+01</td></td></td>	2 <td>S20584<td>DNA-directed RNA poly 2.63e+01</td></td>	S20584 <td>DNA-directed RNA poly 2.63e+01</td>	DNA-directed RNA poly 2.63e+01
28 <td>55<td>57.9<td>227<td>2<td>A24911<td>prolactin-like protein 2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>227<td>2<td>A24911<td>prolactin-like protein 2.63e+01</td></td></td></td></td>	57.9 <td>227<td>2<td>A24911<td>prolactin-like protein 2.63e+01</td></td></td></td>	227 <td>2<td>A24911<td>prolactin-like protein 2.63e+01</td></td></td>	2 <td>A24911<td>prolactin-like protein 2.63e+01</td></td>	A24911 <td>prolactin-like protein 2.63e+01</td>	prolactin-like protein 2.63e+01
29 <td>55<td>57.9<td>305<td>2<td>C64864<td>hypothetical protein 2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>305<td>2<td>C64864<td>hypothetical protein 2.63e+01</td></td></td></td></td>	57.9 <td>305<td>2<td>C64864<td>hypothetical protein 2.63e+01</td></td></td></td>	305 <td>2<td>C64864<td>hypothetical protein 2.63e+01</td></td></td>	2 <td>C64864<td>hypothetical protein 2.63e+01</td></td>	C64864 <td>hypothetical protein 2.63e+01</td>	hypothetical protein 2.63e+01
30 <td>55<td>57.9<td>453<td>2<td>S59436<td>hypothetical protein 2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>453<td>2<td>S59436<td>hypothetical protein 2.63e+01</td></td></td></td></td>	57.9 <td>453<td>2<td>S59436<td>hypothetical protein 2.63e+01</td></td></td></td>	453 <td>2<td>S59436<td>hypothetical protein 2.63e+01</td></td></td>	2 <td>S59436<td>hypothetical protein 2.63e+01</td></td>	S59436 <td>hypothetical protein 2.63e+01</td>	hypothetical protein 2.63e+01
31 <td>55<td>57.9<td>462<td>2<td>A42401<td>macrophage elastase (2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>462<td>2<td>A42401<td>macrophage elastase (2.63e+01</td></td></td></td></td>	57.9 <td>462<td>2<td>A42401<td>macrophage elastase (2.63e+01</td></td></td></td>	462 <td>2<td>A42401<td>macrophage elastase (2.63e+01</td></td></td>	2 <td>A42401<td>macrophage elastase (2.63e+01</td></td>	A42401 <td>macrophage elastase (2.63e+01</td>	macrophage elastase (2.63e+01
32 <td>55<td>57.9<td>911<td>2<td>S28098<td>stef protein - f1s10 2.63e+01</td></td></td></td></td></td>	55 <td>57.9<td>911<td>2<td>S28098<td>stef protein - f1s10 2.63e+01</td></td></td></td></td>	57.9 <td>911<td>2<td>S28098<td>stef protein - f1s10 2.63e+01</td></td></td></td>	911 <td>2<td>S28098<td>stef protein - f1s10 2.63e+01</td></td></td>	2 <td>S28098<td>stef protein - f1s10 2.63e+01</td></td>	S28098 <td>stef protein - f1s10 2.63e+01</td>	stef protein - f1s10 2.63e+01
33 <td>54<td>56.8<td>154<td>2<td>S03242<td>hypothetical protein 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>154<td>2<td>S03242<td>hypothetical protein 3.75e+01</td></td></td></td></td>	56.8 <td>154<td>2<td>S03242<td>hypothetical protein 3.75e+01</td></td></td></td>	154 <td>2<td>S03242<td>hypothetical protein 3.75e+01</td></td></td>	2 <td>S03242<td>hypothetical protein 3.75e+01</td></td>	S03242 <td>hypothetical protein 3.75e+01</td>	hypothetical protein 3.75e+01
34 <td>54<td>56.8<td>179<td>2<td>I40594<td>DNA-directed DNA poly 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>179<td>2<td>I40594<td>DNA-directed DNA poly 3.75e+01</td></td></td></td></td>	56.8 <td>179<td>2<td>I40594<td>DNA-directed DNA poly 3.75e+01</td></td></td></td>	179 <td>2<td>I40594<td>DNA-directed DNA poly 3.75e+01</td></td></td>	2 <td>I40594<td>DNA-directed DNA poly 3.75e+01</td></td>	I40594 <td>DNA-directed DNA poly 3.75e+01</td>	DNA-directed DNA poly 3.75e+01
35 <td>54<td>56.8<td>189<td>2<td>S59264<td>hypothetical protein 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>189<td>2<td>S59264<td>hypothetical protein 3.75e+01</td></td></td></td></td>	56.8 <td>189<td>2<td>S59264<td>hypothetical protein 3.75e+01</td></td></td></td>	189 <td>2<td>S59264<td>hypothetical protein 3.75e+01</td></td></td>	2 <td>S59264<td>hypothetical protein 3.75e+01</td></td>	S59264 <td>hypothetical protein 3.75e+01</td>	hypothetical protein 3.75e+01
36 <td>54<td>56.8<td>342<td>2<td>S51402<td>probable membrane pro 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>342<td>2<td>S51402<td>probable membrane pro 3.75e+01</td></td></td></td></td>	56.8 <td>342<td>2<td>S51402<td>probable membrane pro 3.75e+01</td></td></td></td>	342 <td>2<td>S51402<td>probable membrane pro 3.75e+01</td></td></td>	2 <td>S51402<td>probable membrane pro 3.75e+01</td></td>	S51402 <td>probable membrane pro 3.75e+01</td>	probable membrane pro 3.75e+01
37 <td>54<td>56.8<td>421<td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td></td>	421 <td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td>	2 <td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td>	S187A <td>Seryl-trna synthetase 3.75e+01</td>	Seryl-trna synthetase 3.75e+01
38 <td>54<td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td>	421 <td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td>	2 <td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td>	S187B <td>Seryl-trna synthetase 3.75e+01</td>	Seryl-trna synthetase 3.75e+01
39 <td>54<td>56.8<td>421<td>2<td>S38948<td>Seryl-trna synthetase (3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S38948<td>Seryl-trna synthetase (3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S38948<td>Seryl-trna synthetase (3.75e+01</td></td></td></td>	421 <td>2<td>S38948<td>Seryl-trna synthetase (3.75e+01</td></td></td>	2 <td>S38948<td>Seryl-trna synthetase (3.75e+01</td></td>	S38948 <td>Seryl-trna synthetase (3.75e+01</td>	Seryl-trna synthetase (3.75e+01
40 <td>54<td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td>	421 <td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td>	2 <td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td>	S187B <td>Seryl-trna synthetase 3.75e+01</td>	Seryl-trna synthetase 3.75e+01
41 <td>54<td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td>	421 <td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td>	2 <td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td>	S187B <td>Seryl-trna synthetase 3.75e+01</td>	Seryl-trna synthetase 3.75e+01
42 <td>54<td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td>	421 <td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td>	2 <td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td>	S187B <td>Seryl-trna synthetase 3.75e+01</td>	Seryl-trna synthetase 3.75e+01
43 <td>54<td>56.8<td>421<td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td></td>	421 <td>2<td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td></td>	2 <td>S187A<td>Seryl-trna synthetase 3.75e+01</td></td>	S187A <td>Seryl-trna synthetase 3.75e+01</td>	Seryl-trna synthetase 3.75e+01
44 <td>54<td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td></td>	56.8 <td>421<td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td></td>	421 <td>2<td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td></td>	2 <td>S187B<td>Seryl-trna synthetase 3.75e+01</td></td>	S187B <td>Seryl-trna synthetase 3.75e+01</td>	Seryl-trna synthetase 3.75e+01
45 <td>54<td>56.8<td>752<td>2<td>S51866<td>Hpr1 protein - yeast 3.75e+01</td></td></td></td></td></td>	54 <td>56.8<td>752<td>2<td>S51866<td>Hpr1 protein - yeast 3.75e+01</td></td></td></td></td>	56.8 <td>752<td>2<td>S51866<td>Hpr1 protein - yeast 3.75e+01</td></td></td></td>	752 <td>2<td>S51866<td>Hpr1 protein - yeast 3.75e+01</td></td></td>	2 <td>S51866<td>Hpr1 protein - yeast 3.75e+01</td></td>	S51866 <td>Hpr1 protein - yeast 3.75e+01</td>	Hpr1 protein - yeast 3.75e+01

ALIGNMENTS

RESULT 1
ENTRY 12WE #type complete
TITLE parathyroid hormone (residues 4-37) - human
ALTERNATE_NAMES HPTH(4-37)
PDB_TITLE structure of human parathyroid hormone fragment 4-37, NMR 10 structures
ORGANISM #formal_name Homo sapiens #common_name man
REFERENCE A67860
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WE
REFERENCE TN001721
#authors Marx, U.C.
#book In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS hormone
FEATURE 15-25
SUMMARY #region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 95; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.21e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 21 LRKKLDVHNFEVA 33
QY 1 LRKKLDVHNFEVA 13
RESULT 2
ENTRY 12WG #type complete
TITLE parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED - synthetic
ALTERNATE_NAMES n-succinyl-1-hPTH(4-37)
PDB_TITLE succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM #formal_name synthetic
REFERENCE A67743
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WG
REFERENCE TN003319
#authors Marx, U.C.
#book In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT Resolution: not applicable

Thu Jul 30 13:38:09 1998

US-08-817-547A-28.rpr

Page 2

COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE
2-9
15-25
SUMMARY
#region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 95; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.21e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 21 LKKLQDVHNFVA 33
|||
OY 1 LKKLQDVHNFVA 13






Search completed: Thu Jul 30 11:04:18 1998
Job time : 29 secs.

Search completed: Thu Jul 30 11:02:48 1998
Job time : 7 secs.

OC EUTHERIA; ARTIODACTYLIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T., JR., RICH A.;
RN PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RP [2]
RX SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RL COHN D.V.;
RN PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RL AUBRACH G.D., POTTS J.T., JR.;
RN HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RP [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREMER H.B., JR., ROMAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFTOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.;
RN PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; J00106; G85; -;
DR EMBL; J00023; G163641; -;
DR EMBL; J00024; G163643; -;
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K0138; G163647; -;
DR EMBL; M25082; G163645; -;
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31 PARATHYROID HORMONE.
FT CHAIN 32 115 V -> G (IN REF. 4).
FT CONFLICT 106 106
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 95; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.50e-09;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 55 LRKKLDVHNHFA 67
OY 1 LRKKLDVHNHFA 13

RN [2]
 RP COMPLETE GENOME.
 RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
 RA RODRIGUEZ J.F., VINUELA E.;
 RL VIROLOGY 208:249-278(1995).
 CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
 CC PROTEINS P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.
 DR EMBL: Z22777; G394709; -.
 DR EMBL: U18466; G780461; -.
 KW POLYPROTEIN.
 SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3C0A CRC32;

Query Match 69.5% Score 66; DB 11; Length 2475;
 Best Local Similarity 75.0%; Pred. No. 4.93e-02;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1944 LKRLQDVISFV 1955
 QY 1 LKRLQDVHNFV 12

Search completed: Thu Jul 30 11:03:33 1998
 Job time : 27 secs.

(xL)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:07:12 1998; MasPar time 2.78 Seconds
66.125 Million cell updates/sec
Tabular output not generated.

```

Title:	>US-08-817-547A-29
Description:	(1-12) from US08817547A.pep
Perfect Score:	91
Sequence:	1 LRRK1QDVHNFV 12

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database: a-geneseq31-2
1:part1 2:part3 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27
```

Statistics: Mean 18.683; Variance 61.585; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	91	100.0	36	9	R58213	[A1a19]-hPTH(1-36)-NH	1.17e-02
2	91	100.0	36	9	R58213	[D-Seq17]-hPTH(1-36)-	1.17e-02
3	91	100.0	36	9	R58286	[D-Leu24]-hPTH(1-36)-	1.17e-02
4	91	100.0	36	9	R58052	[L8,A17,Q18,A19]-hPTH	1.17e-02
5	91	100.0	44	26	P30015	Human parathyroid hor	1.17e-02
6	91	100.0	47	25	W21946	Fusion protein compri	1.17e-02
7	91	100.0	48	27	M25687	Human parathyroid hor	1.17e-02
8	91	100.0	84	4	R23545	Bovine parathyroid ho	1.17e-02
9	91	100.0	84	4	R23554	Bovine parathyroid ho	1.17e-02
10	91	100.0	84	4	R23520	Bovine parathyroid ho	1.17e-02
11	91	100.0	84	4	R23463	Porcine parathyroid h	1.17e-02
12	91	100.0	84	4	R23350	Bovine parathyroid ho	1.17e-02
13	91	100.0	84	4	R23522	Human parathyroid hor	1.17e-02
14	91	100.0	84	4	R21342	Human parathyroid hor	1.17e-02
15	91	100.0	84	4	R23373	Bovine parathyroid ho	1.17e-02
16	91	100.0	84	4	R23330	Human parathyroid hor	1.17e-02
17	91	100.0	84	4	R21347	Human parathyroid hor	1.17e-02
18	91	100.0	84	4	R23547	Human parathyroid hor	1.17e-02
19	91	100.0	84	5	R23561	Oxidation resistant p	1.17e-02

20	91	100.0	84	5	R29566	Oxidant resistant [1.17e-02
21	91	100.0	84	4	R23518	Bovine parathyroid ho	1.17e-02
22	91	100.0	84	4	R23432	Porcine parathyroid h	1.17e-02
23	91	100.0	84	4	R23364	Bovine parathyroid ho	1.17e-02
24	91	100.0	84	4	R23365	Bovine parathyroid ho	1.17e-02
25	91	100.0	84	25	W29420	Human parathyroid hor	1.17e-02
26	91	100.0	84	4	R21254	Human parathyroid hor	1.17e-02
27	91	100.0	84	4	R21255	Human parathyroid hor	1.17e-02
28	91	100.0	84	4	R23439	Porcine parathyroid h	1.17e-02
29	91	100.0	84	4	R21165	Human parathyroid hor	1.17e-02
30	91	100.0	84	4	R23243	Human parathyroid hor	1.17e-02
31	91	100.0	84	4	R21239	Human parathyroid hor	1.17e-02
32	91	100.0	84	4	R21232	Human parathyroid hor	1.17e-02
33	91	100.0	84	4	R21233	Human parathyroid hor	1.17e-02
34	91	100.0	84	4	R23529	Bovine parathyroid ho	1.17e-02
35	91	100.0	84	4	R23529	Human parathyroid hor	1.17e-02
36	91	100.0	84	4	R21217	Human parathyroid hor	1.17e-02
37	91	100.0	84	4	R23266	Bovine parathyroid ho	1.17e-02
38	91	100.0	84	4	R23279	Bovine parathyroid ho	1.17e-02
39	91	100.0	84	4	R23278	Bovine parathyroid ho	1.17e-02
40	91	100.0	84	4	R21214	Human parathyroid hor	1.17e-02
41	91	100.0	84	4	R23417	Porcine parathyroid h	1.17e-02
42	91	100.0	84	4	R21194	Human parathyroid hor	1.17e-02
43	91	100.0	84	4	R21193	Human parathyroid hor	1.17e-02
44	91	100.0	102	4	P40252	Protein including hum	1.17e-02
45	91	100.0	115	4	P40209	Sequence of prepropr	1.17e-02

ALIGNMENTS

ID	RESULT	1
AC	RS8214	standard; peptide; 36 AA.
DT	20-SEP-1994	(first entry)
DE	[1a19]-hPTH(1-36)-NH ₂ .	
KW	Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; hypoparathyroidism.	
KW	hypoparathyroidism.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	modified_site	36
FT		/note- "in amide form"
PN	GB2269176-A.	
PD	02-FEB-1994.	
PE	12-JUL-1993: 014384.	
PR	15-JUL-1992: GB-015009.	
PR	18-DEC-1992: GB-026415.	
PR	23-DEC-1992: GB-026859.	
PR	23-DEC-1992: GB-026861.	
PR	28-JAN-1993: GB-001691.	
PR	28-JAN-1993: GB-001692.	
PR	14-APR-1993: GB-007673.	
PR	19-APR-1993: GB-008033.	
PA	(SANO) SANDOZ LTD.	
PA	(BAUE/) BAUER W.	
PA	(SANO) SANDOZ PATENT GMBH.	
PA	(SANO) SANDOZ-ERFINDUNGEN VERN GES MBH.	
PI	Albert R, Bauer W, Breckenridge R, Cardinaux F;	
PI	Gombert F, Gram H, Lewis I, Ramage P, Schneider H;	
PI	Waelchli R, Rainer A;	
DR	WPI: 94-018352/03.	
PT	New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.	
PS	Example 212: Page 44: 92pp: English.	
CC	This peptide is an example of a highly genetic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism.	
CC	hypoparathyroidism.	
SO	Sequence	36 AA;
Query Match	100.0%;	Score 91; DB 9; Length 36;
Best Local Similarity	100.0%;	Pred. No. 1.17e-02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLQGVHNFV 35

OY 1 LKKLQGVHNFV 12

RESULT 2

ID R58213 standard; peptide: 36 AA.

AC R58213;

DT 20-SEP-1994 (first entry)

DE [D-Ser17]-hPTH(1-36)-NH₂.

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteoporosis;

KW hypoparathyroidism.

OS Synthetic.

FT Key

FT misc_difference 17

FT modified_site 36

FT /note= "D-form residue."

FT /note= "in amide form"

GB2269176-A.

02-FEB-1994.

12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.

(SANO) SANDOZ LTD.

(BAUE/) BAUER W.

(SANO) SANDOZ PATENT GMBH.

(SANO) SANDOZ-EPRENDUNGEN VERW GES MBH.

Albert R, Bauer W, Breckenridge R, Cardinaux F;

Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

Maechli R, Ralner A;

WPI: 94-018352/03.

PT New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

PS Example 211; Page 44; 92pp; English.

CC This peptide is an example of a highly generic formula covering

CC parathyroid hormone variants useful for treating or preventing bone

CC conditions associated with calcium depletion/resorption, in cases

CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

Sequence 36 AA;

Query Match 100.0%; Score 91; DB 9; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.17e-02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLQGVHNFV 35

OY 1 LKKLQGVHNFV 12

Search completed: Thu Jul 30 11:07:36 1998

Job time : 24 secs.

WIDEORH
(TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:06:37 1998; MasPar time 3.31 Seconds
Tabular output not generated. 132.368 Million cell updates/sec

Title: >US-08-817-547A-29
Description: (1-12) from US08817547A.dep
Perfect Score: 91
Sequence: 1 LRRKLDVHNFV 12

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.786; Variance 40.708; scale 0.633

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	91	100.0	34	5 12WE	parathyroid hormone (4.58e-06	
2	91	100.0	34	5 12WG	parathyroid hormone (4.58e-06	
3	91	100.0	34	5 12WF	parathyroid hormone (4.58e-06	
4	91	100.0	34	5 12WD	parathyroid hormone (4.58e-06	
5	91	100.0	36	5 12WB	parathyroid hormone (4.58e-06	
6	91	100.0	37	5 12WC	parathyroid hormone (4.58e-06	
7	91	100.0	37	5 12WD	parathyroid hormone (4.58e-06	
8	91	100.0	37	5 12WB	parathyroid hormone (4.58e-06	
9	91	100.0	37	5 12WC	parathyroid hormone (4.58e-06	
10	91	100.0	37	5 12WD	parathyroid hormone (4.58e-06	
11	91	100.0	37	5 12WB	parathyroid hormone (4.58e-06	
12	91	100.0	37	5 12WC	parathyroid hormone (4.58e-06	
13	84	92.3	34	5 12WA	parathyroid hormone (1.16e-04	
14	84	92.3	34	5 12WB	parathyroid hormone (1.16e-04	
15	81	89.0	105	2 151851	cyclic parathyroid hormone (4.52e-04	
16	66	72.5	2475	2 535307	parathyroid hormone - 2.87e-01	
17	60	65.9	444	2 509881	citrate transport pro 3.14e+00	
18	58	63.7	183	2 542547	glucose-1-phosphate a 6.77e+00	
19	58	63.7	330	2 151545	myc protein - African 6.77e+00	
20	57	62.6	419	1 TVXLMC	transforming protein 6.77e+00	
21	57	62.6	281	2 S41854	phosphoprotein phosph 9.88e+00	
22	57	62.6	525	2 C64313	hypothetical protein 9.88e+00	
23	55	60.4	119	2 A34937	parathyroid hormone p 2.08e+01	

24	55	60.4	305	2	C64864	hypothetical protein 2.08e+01
25 <td>55<td>60.4<td>445<td>2<td>S43492<td>surface antigen - hep 2.08e+01</td></td></td></td></td></td>	55 <td>60.4<td>445<td>2<td>S43492<td>surface antigen - hep 2.08e+01</td></td></td></td></td>	60.4 <td>445<td>2<td>S43492<td>surface antigen - hep 2.08e+01</td></td></td></td>	445 <td>2<td>S43492<td>surface antigen - hep 2.08e+01</td></td></td>	2 <td>S43492<td>surface antigen - hep 2.08e+01</td></td>	S43492 <td>surface antigen - hep 2.08e+01</td>	surface antigen - hep 2.08e+01
26 <td>55<td>60.4<td>453<td>2<td>S59436<td>hypothetical protein 2.08e+01</td></td></td></td></td></td>	55 <td>60.4<td>453<td>2<td>S59436<td>hypothetical protein 2.08e+01</td></td></td></td></td>	60.4 <td>453<td>2<td>S59436<td>hypothetical protein 2.08e+01</td></td></td></td>	453 <td>2<td>S59436<td>hypothetical protein 2.08e+01</td></td></td>	2 <td>S59436<td>hypothetical protein 2.08e+01</td></td>	S59436 <td>hypothetical protein 2.08e+01</td>	hypothetical protein 2.08e+01
27 <td>55<td>60.4<td>462<td>2<td>A42401<td>macrophage elastase (2.08e+01</td></td></td></td></td></td>	55 <td>60.4<td>462<td>2<td>A42401<td>macrophage elastase (2.08e+01</td></td></td></td></td>	60.4 <td>462<td>2<td>A42401<td>macrophage elastase (2.08e+01</td></td></td></td>	462 <td>2<td>A42401<td>macrophage elastase (2.08e+01</td></td></td>	2 <td>A42401<td>macrophage elastase (2.08e+01</td></td>	A42401 <td>macrophage elastase (2.08e+01</td>	macrophage elastase (2.08e+01
28 <td>55<td>60.4<td>911<td>2<td>S28098<td>st66 protein - fission 2.08e+01</td></td></td></td></td></td>	55 <td>60.4<td>911<td>2<td>S28098<td>st66 protein - fission 2.08e+01</td></td></td></td></td>	60.4 <td>911<td>2<td>S28098<td>st66 protein - fission 2.08e+01</td></td></td></td>	911 <td>2<td>S28098<td>st66 protein - fission 2.08e+01</td></td></td>	2 <td>S28098<td>st66 protein - fission 2.08e+01</td></td>	S28098 <td>st66 protein - fission 2.08e+01</td>	st66 protein - fission 2.08e+01
29 <td>54<td>59.3<td>102<td>2<td>S53076<td>probable membrane pro 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>102<td>2<td>S53076<td>probable membrane pro 2.99e+01</td></td></td></td></td>	59.3 <td>102<td>2<td>S53076<td>probable membrane pro 2.99e+01</td></td></td></td>	102 <td>2<td>S53076<td>probable membrane pro 2.99e+01</td></td></td>	2 <td>S53076<td>probable membrane pro 2.99e+01</td></td>	S53076 <td>probable membrane pro 2.99e+01</td>	probable membrane pro 2.99e+01
30 <td>54<td>59.3<td>154<td>2<td>S03242<td>hypothetical protein 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>154<td>2<td>S03242<td>hypothetical protein 2.99e+01</td></td></td></td></td>	59.3 <td>154<td>2<td>S03242<td>hypothetical protein 2.99e+01</td></td></td></td>	154 <td>2<td>S03242<td>hypothetical protein 2.99e+01</td></td></td>	2 <td>S03242<td>hypothetical protein 2.99e+01</td></td>	S03242 <td>hypothetical protein 2.99e+01</td>	hypothetical protein 2.99e+01
31 <td>54<td>59.3<td>179<td>2<td>I40594<td>DNA-directed DNA poly 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>179<td>2<td>I40594<td>DNA-directed DNA poly 2.99e+01</td></td></td></td></td>	59.3 <td>179<td>2<td>I40594<td>DNA-directed DNA poly 2.99e+01</td></td></td></td>	179 <td>2<td>I40594<td>DNA-directed DNA poly 2.99e+01</td></td></td>	2 <td>I40594<td>DNA-directed DNA poly 2.99e+01</td></td>	I40594 <td>DNA-directed DNA poly 2.99e+01</td>	DNA-directed DNA poly 2.99e+01
32 <td>54<td>59.3<td>189<td>2<td>S59264<td>hypothetical protein 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>189<td>2<td>S59264<td>hypothetical protein 2.99e+01</td></td></td></td></td>	59.3 <td>189<td>2<td>S59264<td>hypothetical protein 2.99e+01</td></td></td></td>	189 <td>2<td>S59264<td>hypothetical protein 2.99e+01</td></td></td>	2 <td>S59264<td>hypothetical protein 2.99e+01</td></td>	S59264 <td>hypothetical protein 2.99e+01</td>	hypothetical protein 2.99e+01
33 <td>54<td>59.3<td>342<td>2<td>S51402<td>probable membrane pro 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>342<td>2<td>S51402<td>probable membrane pro 2.99e+01</td></td></td></td></td>	59.3 <td>342<td>2<td>S51402<td>probable membrane pro 2.99e+01</td></td></td></td>	342 <td>2<td>S51402<td>probable membrane pro 2.99e+01</td></td></td>	2 <td>S51402<td>probable membrane pro 2.99e+01</td></td>	S51402 <td>probable membrane pro 2.99e+01</td>	probable membrane pro 2.99e+01
34 <td>54<td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SERB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
35 <td>54<td>59.3<td>421<td>5<td>1SRXB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SRXB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SRXB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SRXB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SRXB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SRXB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
36 <td>54<td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SERB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
37 <td>54<td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SERB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
38 <td>54<td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SERB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
39 <td>54<td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SERB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
40 <td>54<td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SERB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
41 <td>54<td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td></td>	59.3 <td>421<td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td></td>	421 <td>5<td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td></td>	5 <td>1SERB<td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td></td>	1SERB <td>Seryl-<i>t</i>-RNA synthetase 2.99e+01</td>	Seryl- <i>t</i> -RNA synthetase 2.99e+01
42 <td>54<td>59.3<td>752<td>2<td>S51866<td>HPRI protein - yeast 2.99e+01</td></td></td></td></td></td>	54 <td>59.3<td>752<td>2<td>S51866<td>HPRI protein - yeast 2.99e+01</td></td></td></td></td>	59.3 <td>752<td>2<td>S51866<td>HPRI protein - yeast 2.99e+01</td></td></td></td>	752 <td>2<td>S51866<td>HPRI protein - yeast 2.99e+01</td></td></td>	2 <td>S51866<td>HPRI protein - yeast 2.99e+01</td></td>	S51866 <td>HPRI protein - yeast 2.99e+01</td>	HPRI protein - yeast 2.99e+01
43 <td>53<td>58.2<td>348<td>2<td>S45890<td>ODP1 protein - yeast 4.29e+01</td></td></td></td></td></td>	53 <td>58.2<td>348<td>2<td>S45890<td>ODP1 protein - yeast 4.29e+01</td></td></td></td></td>	58.2 <td>348<td>2<td>S45890<td>ODP1 protein - yeast 4.29e+01</td></td></td></td>	348 <td>2<td>S45890<td>ODP1 protein - yeast 4.29e+01</td></td></td>	2 <td>S45890<td>ODP1 protein - yeast 4.29e+01</td></td>	S45890 <td>ODP1 protein - yeast 4.29e+01</td>	ODP1 protein - yeast 4.29e+01
44 <td>53<td>58.2<td>500<td>2<td>C64043<td>citrate (pro-3S)-lyase 4.29e+01</td></td></td></td></td></td>	53 <td>58.2<td>500<td>2<td>C64043<td>citrate (pro-3S)-lyase 4.29e+01</td></td></td></td></td>	58.2 <td>500<td>2<td>C64043<td>citrate (pro-3S)-lyase 4.29e+01</td></td></td></td>	500 <td>2<td>C64043<td>citrate (pro-3S)-lyase 4.29e+01</td></td></td>	2 <td>C64043<td>citrate (pro-3S)-lyase 4.29e+01</td></td>	C64043 <td>citrate (pro-3S)-lyase 4.29e+01</td>	citrate (pro-3S)-lyase 4.29e+01
45 <td>53<td>58.2<td>569<td>2<td>S62851<td>MG397 homolog D02_orf 4.29e+01</td></td></td></td></td></td>	53 <td>58.2<td>569<td>2<td>S62851<td>MG397 homolog D02_orf 4.29e+01</td></td></td></td></td>	58.2 <td>569<td>2<td>S62851<td>MG397 homolog D02_orf 4.29e+01</td></td></td></td>	569 <td>2<td>S62851<td>MG397 homolog D02_orf 4.29e+01</td></td></td>	2 <td>S62851<td>MG397 homolog D02_orf 4.29e+01</td></td>	S62851 <td>MG397 homolog D02_orf 4.29e+01</td>	MG397 homolog D02_orf 4.29e+01

ALIGNMENTS

RESULT	ENTRY	12WE	#type complete
TITLE	parathyroid hormone (residues 4-37) - human		
ALTERNATE_NAMES	HPTH(4-37)		
PDB_TITLE	structure of human parathyroid hormone fragment 4-37, NMR 10 structures		
ORGANISM	#formal_name Homo sapiens #common_name man		
REFERENCE	A67860 Roesch, P.; Marx, U.C.		
#authors	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WE		
REFERENCE	TN001721		
#authors	Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loesung, pp. 0, Bayreuth: University of Bayreuth (Thesis), 1996		
COMMENT	Resolution: not applicable		
KEYWORDS	hormone		
FEATURE			
SUMMARY	#region helix (right hand alpha)		
	#length 34 #molecular-weight 4128 #checksum 5508		
Query Match	100.0%; Score 91; DB 5; Length 34;		
Best Local Similarity	100.0%; Pred. No. 4.58e-06;		
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	21 LRRKLDVHNFV 32		
QY	1 LRRKLDVHNFV 12		
RESULT	2		
ENTRY	12WG	#type complete	
TITLE	parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -		
ALTERNATE_NAMES	n-succinyl-hPTH(4-37)		
PDB_TITLE	succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM	#formal_name synthetic		
REFERENCE	A67743 Roesch, P.; Marx, U.C.		
#authors	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WG		
REFERENCE	TN003319		
#authors	Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loesung, pp. 0, Bayreuth: University of Bayreuth (Thesis), 1996		
COMMENT	Resolution: not applicable		

Thu Jul 30 13:38:10 1998

US-08-817-547A-29.rpr

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COMMENT      Determination: NMR
KEYWORDS      disease mutation: hormone; signal
FEATURES      2-9
              15-25
SUMMARY      #region helix (right hand alpha)\
              #region helix (right hand alpha)
              #length 34 #molecular-weight 4128 #checksum 5508
Query Match  100.0%; Score 91; DB 5; Length 34;
Best Local Similarity 100.0%; Pred.No. 4.58e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 21 LRRK1QDVHNFV 32
OY 1 LRRK1QDVHNFV 12
```

Search completed: Thu Jul 30 11:06:55 1998
Job time : 18 secs.

WISCONSIN

(TM)

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MSPrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:06:12 1998; MasPar time 2.30 Seconds
Tabular output not generated. 130.665 Million cell updates/sec

Title: >US-08-817-547A-29
Description: (1-12) from US08817547A.pep
Perfect Score: 91
Sequence: 1 LRRKKIQDVHNFV 12

Scoring table:
Gap 15
PAM 150

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 27.047; Variance 34.136; scale 0.792

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	91	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.71e-08
2	91	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.71e-08
3	91	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.71e-08
4	91	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.71e-08
5	91	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	4.71e-08
6	60	65.9	444	1	CITL_KIEPN PARATHYROID HORMONE PR	5.45e-01
7	58	63.7	184	1	GLC2_AATH GLUCOSE-1-PHOSPHATE AD	1.36e+00
8	58	63.7	419	1	MYC1_XENLA MYC 1 PROTO-ONCOGENE P	2.14e+00
9	57	62.6	281	1	P2C1_YEAST PROTEIN PHOSPHATASE 2C	2.14e+00
10	57	62.6	525	1	Y107_METLA HYPOHETICAL PROTEIN M	2.14e+00
11	55	60.4	119	1	PTHY_CHICK PARATHYROID HORMONE PR	5.16e+00
12	55	60.4	162	1	Y4XD_RHISN HYPOHETICAL 18.0 KD P	5.16e+00
13	55	60.4	305	1	HLVE_ECOLI HEMOLYSIN E (HEMOLYSIN	5.16e+00
14	55	60.4	462	1	COGM_MOUSE MACROPHAGE METALLOELAS	5.16e+00
15	55	60.4	911	1	STB6_SCHPO STE6 PROTEIN.	5.16e+00
16	55	60.4	1053	1	UBA3_WHEAT UBIQUITIN-ACTIVATING E	5.16e+00
17	54	59.3	102	1	YMB8_YEAST HYPOHETICAL 11.8	7.94e+00
18	54	59.3	154	1	Y1K7_SESV1 HYPOHETICAL 17.8 KD P	7.94e+00
19	54	59.3	189	1	YNOO_YEAST VERY HYPOHETICAL 21.7	7.94e+00
20	54	59.3	233	1	DP3E_BUCAP DNA POLYMERASE III, EP	7.94e+00
21	54	59.3	421	1	SYS_THETH SERYL-TRNA SYNTHETASE	7.94e+00
22	54	59.3	752	1	HPRI_YEAST HPRI PROTEIN.	7.94e+00
23	54	59.3	926	1	KINH_NEUCR KINESIN HEAVY CHAIN.	7.94e+00

RESULT	ID	PTHY_BOVIN	STANDARD:	PTHY	115 AA.	ALIGNMENTS
AC	P01268:					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; ARTIODACTYLA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., MCDEVITT B.E., MAJZUB J.A., NATHANS J., SHARP P.A.,					
RA	KRONENBERG H.M., KEMPERS B.,					
RA	POTTS J.T. JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., KEMPERS B.,					
RA	MEADINE: 82037785.					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPERS B.,					
RA	GENE 28:319-329(1984).					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RA	MEADINE: 84262483.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPERS B.,					
RA	MEADINE: 74142666.					
RA	HAMILTON J.W., NISALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,					
RA	CORN D.V.,					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).					
RN	[6]					
RP	SEQUENCE OF 32-115.					
RA	MEADINE: 71076162.					
RA	NISALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,					
RA	AUBACH G.D., POTTS J.T. JR.,					
RL	HOPPE-SEYLER S.Z. PHYSTOL. CHEM. 351:1586-1588(1970).					
RN	[7]					
RP	SEQUENCE OF 32-115.					
RA	MEADINE: 71063634.					

Thu Jul 30 13:38:10 1998

US-08-817-547A-29.rsp

Search completed: Thu Jul 30 11:06:18 1998
Job time : 6 secs.

Page 2

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RA BREMER H.B. JR., RONAN R.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).  
RN [8]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE: 71091588.  
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NALL H.D., SAUER R.,  
RL DEFOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.,  
CC PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
DR BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL: J00106; G85.  
DR EMBL: J00023; G163641;  
DR EMBL: J00024; G163643;  
DR EMBL: J00024; E18248;  
DR EMBL: J00024; E18250; ALT-SEQ.  
DR EMBL: K01938; G163647;  
DR EMBL: M25082; G163645;  
DR PIR: A01534; PTMO.  
DR PIR: A24949; A24949.  
PROSITE: P500335; PARATHYROID; 1.  
HORMONE; SIGNAL.  
FT PROPER 1 25  
FT CHAIN 26 31  
FT CONFLICT 32 115  
SQ SEQUENCE 106 106 PARATHYROID HORMONE.  
Query Match V -> G (IN REF. 4).  
Best Local Similarity 100.0%;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 55 LRRKLDVHNFV 66  
OY 1 LRRKLDVHNFV 12  
RESULT 2  
ID PTH CANFA STANDARD; PRT: 115 AA.  
AC P52212;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DE PARATHYROID HORMONE (REL. 34, LAST SEQUENCE UPDATE)  
GN PTH.  
OS CANIS FAMILIARIS (DOG).  
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
RN [1]  
SEQUENCE FROM N.A.  
TX TISSUE-PARATHYROID;  
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,  
RL DEVILLE J.W., CAPEN C.C.;  
CC GENE 160:241-243(1995).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
DR BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL: U15662; G558916;  
DR PROSITE: P500335; PARATHYROID; 1.  
FT SIGNAL  
FT PROPER 1 25  
FT CHAIN 26 31  
FT CONFLICT 32 115 BY SIMILARITY.  
SQ SEQUENCE 115 AA; 12957 MW; 16DEDEBC CRC32; PARATHYROID HORMONE.  
Query Match  
Best Local Similarity 100.0%;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 55 LRRKLDVHNFV 66  
OY 1 LRRKLDVHNFV 12
```

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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 11:05:15 1998; MasPar time 3.96 Seconds

Tabular output not generated. 127.714 Million cell updates/sec

Title: >US-08-817-547A-29
Description: (1-12) from US08817547A.pep
Perfect Score: 91
Sequence: 1 LRKKLDVHNFV 12

Scoring table:
PAM 150
Gap 15

Searched: 140542 segs. 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:
sptemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 25.804; Variance 33.788; scale 0.764

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	81	89.0	105	10	PARATHYROID HORMONE (F	1.73e-05
2	66	72.5	2475	11	POLYPROTEIN PP220.	3.90e-02
3	61	67.0	207	11	ORF36L.	4.26e-01
4	59	64.8	320	9	HYPOTHETICAL PROTEIN I	1.07e+00
5	58	63.7	330	12	MYC PROTEIN (FRAGMENT)	1.69e+00
6	58	63.7	591	3	F52E10.5 (FRAGMENT).	1.69e+00
7	58	63.7	1291	2	MRNA (K1A0067) FOR OR	1.69e+00
8	57	62.6	299	3	SIMILAR TO SER/THR PRO	2.65e+00
9	57	62.6	1077	8	UBIQUITIN-ACTIVATING E	2.65e+00
10	56	61.5	1080	8	UBIQUITIN-ACTIVATING E	4.14e+00
11	55	60.4	445	11	PRE S-S ORF.	6.42e+00
12	55	60.4	453	1	HYPOTHETICAL 50.0 KD P	6.42e+00
13	55	60.4	1167	10	ZINC FINGER PROTEIN (F	6.42e+00
14	55	60.4	1186	10	ZINC FINGER PROTEIN 10	6.42e+00
15	55	60.4	1459	3	RO9E10.3.	6.42e+00
16	55	60.4	2708	3	CHLOROQUINE RESISTANCE	6.42e+00
17	55	60.4	2742	3	CHLOROQUINE RESISTANCE	6.42e+00
18	55	60.4	2819	3	STRAIN HB3 CG2 (CG2).	6.42e+00
19	54	59.3	265	8	AG15 TYPE 2.	9.91e+00
20	54	59.3	342	1	CHROMOSOME XII COSMID	9.91e+00

21	54	59.3	400	3	026648	TEXTIN B1.	9.91e+00
22	54	59.3	735	3	017750	C06G3.9 PROTEIN.	9.91e+00
23	54	59.3	962	9	P95235	HYPOTHETICAL 104.6 KD	9.91e+00
24	53	58.2	232	9	P95776	DNA FOR DDP-RHAMNOSE	1.52e+01
25	53	58.2	373	3	017639	C04G6.2 PROTEIN.	1.52e+01
26	53	58.2	398	8	004471	SIMILAR TO SACCHAROMYC	1.52e+01
27	53	58.2	1744	3	022516	T14G8.1 (FRAGMENT).	1.52e+01
28	53	58.2	2401	3	026216	RHOPTRY PROTEIN (FRAGM	1.52e+01
29	52	57.1	90	3	P91244	COSMID F11G11.	2.32e+01
30	52	57.1	160	9	044535	ORF 3.	2.32e+01
31	52	57.1	279	10	063338	MYOSIN HEAVY CHAIN (AA	2.32e+01
32	52	57.1	485	3	016872	C13A2.5 PROTEIN.	2.32e+01
33	52	57.1	602	9	P94876	OLIGOPEPTIDASE.	2.32e+01
34	52	57.1	621	10	063339	MYOSIN HEAVY CHAIN 21	2.32e+01
35	52	57.1	929	9	032491	PURATIVE N6-ADEININE S	2.32e+01
36	52	57.1	957	9	028565	TYPE I RESTRICTION-MOD	2.32e+01
37	52	57.1	1312	2	092878	RAD50.	2.32e+01
38	52	57.1	1371	3	001777	SIMILAR TO PROTEIN-TYR	2.32e+01
39	52	57.1	1938	10	008639	MYOSIN.	2.32e+01
40	52	57.1	1972	10	008638	MYOSIN.	2.32e+01
41	51	56.0	360	9	034130	HISC.	3.51e+01
42	51	56.0	509	2	013977	MAJOR YO PARANOPLASTI	3.51e+01
43	51	56.0	1354	2	023669	ZK930.1.	3.51e+01
44	51	56.0	1630	12	090724	MYOMESTIN.	3.51e+01
45	51	56.0	2829	12	P70039	ADENOMATOUS POLYPOSIS	3.51e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	105 AA.
AC	063473	01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATUUS NORVEGICUS (RAT).			
OC	EUFAROTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUHAROTA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-THYROID, AND PARATHYROID;			
RA	SCHMELZER H.J., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -			
FT	NON-TER			
SEQ	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;			
Query Match	89.0%;	Score 81;	DB 10;	Length 105;
Best Local Similarity	91.7%;	Pred. No. 1.73e-05;		
Matches	11;	Conservative	0;	Mismatches 1;
Indels	0;	Gaps	0;	
DB	45 LRKKLDVHNFV 56			
OY	1 LRKKLDVHNFV 12			
RESULT	2	PRELIMINARY:	PRT:	2475 AA.
AC	008358	01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)			
DE	POLYPROTEIN PP220.			
GN	CP2475L.			
OS	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).			
OC	VIRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 93327788.			
RA	SIMON-MATEO C., ANDRES G., VINUELA E.;			
RL	EMBO J. 12:2977-2987(1993).			

Thu Jul 30 13:38:11 1998

US-08-817-547A-29.rsp

Page 2

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RN [2]
RP COMPLETE GENOME.
RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RL RODRIGUEZ J.F., VINTELA E.,
CC VIRIOLOGY 208:249-278(1995).
CC -I- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
DR PROTEINS P150, P37, P94 AND P14 OF AFRICAN SWINE FEVER VIRUS.
DR EMBL: Z22777; G394709; -.
KW POLYPROTEIN
SQ SEQUENCE 2475 AA: 281479 MW: 6F4E3C0A CRC32;

Query Match      72.5%  Score 66;  DB 11;  Length 2475;
Best Local Similarity 75.0%  Pred. No. 3,906-02;
Matches 9;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;

Db 1944 LRRKLDVISEV 1955
    ||| ||| :||
OY 1 LRRKLDVHNFV 12

Search completed: Thu Jul 30 11:05:54 1998
Job time : 39 secs.
```

M O S E L L
(TW)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:10:20 1998; Maspar time 2.67 Seconds
63.142 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRKKLQDVHNF 11

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 1538987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.206; Variance 59.063; scale 0.308

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	84	100.0	34 26	R62432	Accelerator peptide b	4.45e-02
2	84	100.0	34 22	W17957	Human parathyroid hor	4.45e-02
3	84	100.0	34 22	W17956	Human parathyroid hor	4.45e-02
4	84	100.0	34 22	W17958	Human parathyroid hor	4.45e-02
5	84	100.0	34 22	W17959	Human parathyroid hor	4.45e-02
6	84	100.0	34 7	R34363	Human parathyroid hor	4.45e-02
7	84	100.0	36 9	R58182	[Nva8]-hPTH(1-36)-NH2	4.45e-02
8	84	100.0	36 9	R58184	[Tyr18]-hPTH(1-36)-NH2	4.45e-02
9	84	100.0	36 9	R58179	[Leu1]-hPTH(1-36)-NH2	4.45e-02
10	84	100.0	36 9	R58069	Isopropyl-[L8,K(Isopr	4.45e-02
11	84	100.0	36 9	R58285	[Ala23]-hPTH(1-36)-NH	4.45e-02
12	84	100.0	36 9	R58074	[L8,Y18]-hPTH(1-36)-O	4.45e-02
13	84	100.0	44 26	P30015	Human parathyroid hor	4.45e-02
14	84	100.0	84 27	W25687	Human parathyroid hor	4.45e-02
15	84	100.0	84 4	R23523	Human parathyroid hor	4.45e-02
16	84	100.0	84 4	R23447	Porcine parathyroid h	4.45e-02
17	84	100.0	84 4	R23253	Bovine parathyroid ho	4.45e-02
18	84	100.0	84 9	R49695	Sequence of variant c	4.45e-02
19	84	100.0	84 4	R23444	Porcine parathyroid h	4.45e-02

20	84	100.0	84 4	R21221	Human parathyroid hor	4.45e-02
21	84	100.0	84 4	R23463	Porcine parathyroid h	4.45e-02
22	84	100.0	84 4	R21201	Human parathyroid hor	4.45e-02
23	84	100.0	84 4	R21200	Human parathyroid hor	4.45e-02
24	84	100.0	84 4	R21203	Human parathyroid hor	4.45e-02
25	84	100.0	84 4	R21202	Human parathyroid hor	4.45e-02
26	84	100.0	84 4	R23376	Bovine parathyroid ho	4.45e-02
27	84	100.0	84 4	R23464	Porcine parathyroid h	4.45e-02
28	84	100.0	84 4	R23366	Bovine parathyroid ho	4.45e-02
29	84	100.0	84 4	R23365	Bovine parathyroid ho	4.45e-02
30	84	100.0	84 4	R23354	Bovine parathyroid ho	4.45e-02
31	84	100.0	84 4	R23545	Bovine parathyroid ho	4.45e-02
32	84	100.0	84 4	R21206	Human parathyroid hor	4.45e-02
33	84	100.0	84 4	R21207	Human parathyroid hor	4.45e-02
34	84	100.0	84 4	R23233	Human parathyroid hor	4.45e-02
35	84	100.0	84 4	R21220	Human parathyroid hor	4.45e-02
36	84	100.0	84 4	R23311	Bovine parathyroid ho	4.45e-02
37	84	100.0	84 4	R23510	Porcine parathyroid h	4.45e-02
38	84	100.0	84 4	R23255	Bovine parathyroid ho	4.45e-02
39	84	100.0	84 5	R29562	Oxidation resistant l	4.45e-02
40	84	100.0	84 5	R28846	Bovine parathyroid ho	4.45e-02
41	84	100.0	84 4	R23380	Bovine parathyroid ho	4.45e-02
42	84	100.0	84 4	R23381	Bovine parathyroid ho	4.45e-02
43	84	100.0	84 4	R23418	Porcine parathyroid h	4.45e-02
44	84	100.0	84 4	R23323	Bovine parathyroid ho	4.45e-02
45	84	100.0	115 4	P40251	Protein sequence incl	4.45e-02

ALIGNMENTS

RESULT 1
ID R62432 standard; peptide; 34 AA.

AC R62432;
DT 31-JUL-1995 (first entry)
DE Accelerator peptide basic region peptide, P-8
KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW Periodontal tissue; regeneration; periodontitis; periodontal pocket;
KW down growth; epithelium; fibre adhesion; cement.
OS Synthetic.

PN J06234653-AA.
PD 23-AUG-1994.
PF 10-FEB-1993; 045998.
PR 10-FEB-1993; JP-045998.
PA (SUNZ) SUNSTAR CHEM IND CO LTD.
DR WPI; 95-157631/21.
PT Accelerator for regenerating periodontal tissue - comprises
PT peptide having 3-34 aminoacid residues having connected basic
PT aminoacid residues
PS Disclosure; Page 3; 7pp; Japanese.
CC The sequences in R62425-36 are peptide fragments of an accelerator
CC protein which contain at least two basic amino acids. The accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerate the growth of periodontal tissue regeneration. The
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC periodontal pocket. The accelerator reduces the down growth of the
CC epithelium and accelerates fibre adhesion and regenerates cement.
SQ Sequence 34 AA;

Query Match 100.0%; Score 84; DB 26; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.45e-02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LRKKLQDVHNF 34
|||||
QY 1 LRKKLQDVHNF 11

RESULT 2
ID W17957 standard; peptide; 34 AA.
AC W17957;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Ala3]hPTH(1-34)NH2.

KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 KW bone fracture.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_site 3 /label= Alb
 FT modified_site 34
 FT /note= "in amide form"
 FT WO9702834-A1.
 PN 30-JAN-1997.
 PD 03-JUL-1996; U11282.
 PF 13-JUL-1995; US-001105.
 PR 06-SEP-1995; US-003305.
 PR 29-MAR-1996; US-626186.
 PA (BIOM-) BIOMESDURE INC.
 PI Dong ZX:
 PI WPI; 97-118819/11.
 PT New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture
 Claim 11: Page -: 33pp; English.
 CC The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 is alpha-aminoisobutyric acid (Alb). In this example the Ser residue at position 3 of the wild-type has been substituted by Alb. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).
 CC N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim.
 CC Sequence 34 AA;
 SQ

Query Match 100.0%; Score 84; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4,45e-02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLGDVHNF 34
 |||||
 QY 1 LKKLQDVHNF 11

Search completed: Thu Jul 30 11:10:35 1998
 Job time : 15 secs.

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:09:33 1998; MasPar time 3.26 Seconds
Tabular output not generated. 123.270 Million cell updates/sec

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRRKLDVHNF 11

Scoring table:
PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:pir13d

Statistics: Mean 25.053; Variance 38.928; scale 0.644

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	84	100.0	34	5	12WG parathyroid hormone 4	4.83e-05
2	84	100.0	34	5	12WF parathyroid hormone 4	4.83e-05
3	84	100.0	34	5	12WR parathyroid hormone 4	4.83e-05
4	84	100.0	34	5	12WE parathyroid hormone 4	4.83e-05
5	84	100.0	34	5	12WA parathyroid hormone 4	4.83e-05
6	84	100.0	34	5	12WD parathyroid hormone 4	4.83e-05
7	84	100.0	34	5	12WB parathyroid hormone 4	4.83e-05
8	84	100.0	34	5	12WC parathyroid hormone 4	4.83e-05
9	84	100.0	34	5	12WP parathyroid hormone 4	4.83e-05
10	84	100.0	34	5	12WQ parathyroid hormone 4	4.83e-05
11	84	100.0	34	5	12WR parathyroid hormone 4	4.83e-05
12	84	100.0	34	5	12WF parathyroid hormone 4	4.83e-05
13	84	100.0	34	5	12WR parathyroid hormone 4	4.83e-05
14	84	100.0	34	5	12WE parathyroid hormone 4	4.83e-05
15	84	100.0	34	5	12WA parathyroid hormone 4	4.83e-05
16	84	100.0	34	5	12WD parathyroid hormone 4	4.83e-05
17	84	100.0	34	5	12WB parathyroid hormone 4	4.83e-05
18	84	100.0	34	5	12WC parathyroid hormone 4	4.83e-05
19	84	100.0	34	5	12WP parathyroid hormone 4	4.83e-05
20	84	100.0	34	5	12WQ parathyroid hormone 4	4.83e-05
21	84	100.0	34	5	12WR parathyroid hormone 4	4.83e-05
22	84	100.0	34	5	12WF parathyroid hormone 4	4.83e-05
23	84	100.0	34	5	12WR parathyroid hormone 4	4.83e-05

24	54	64.3	189	2	S59264	hypothetical protein	1.83e+01
25 <td>54</td> <td>64.3<td>342<td>2</td><td>S51402</td><td>probable membrane pro</td><th>1.83e+01</th></td></td>	54	64.3 <td>342<td>2</td><td>S51402</td><td>probable membrane pro</td><th>1.83e+01</th></td>	342 <td>2</td> <td>S51402</td> <td>probable membrane pro</td> <th>1.83e+01</th>	2	S51402	probable membrane pro	1.83e+01
26 <td>54</td> <td>64.3<td>421<td>2</td><td>S38948</td><td>serine-CRNA ligase (</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>2</td><td>S38948</td><td>serine-CRNA ligase (</td><th>1.83e+01</th></td>	421 <td>2</td> <td>S38948</td> <td>serine-CRNA ligase (</td> <th>1.83e+01</th>	2	S38948	serine-CRNA ligase (1.83e+01
27 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYA</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYA</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYA</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYA	Seryl-trna synthetase	1.83e+01
28 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYB</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYB</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYB</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYB	Seryl-trna synthetase	1.83e+01
29 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYC</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYC</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYC</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYC	Seryl-trna synthetase	1.83e+01
30 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYD</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYD</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYD</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYD	Seryl-trna synthetase	1.83e+01
31 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYE</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYE</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYE</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYE	Seryl-trna synthetase	1.83e+01
32 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYF</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYF</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYF</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYF	Seryl-trna synthetase	1.83e+01
33 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYG</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYG</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYG</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYG	Seryl-trna synthetase	1.83e+01
34 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYH</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYH</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYH</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYH	Seryl-trna synthetase	1.83e+01
35 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYI</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYI</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYI</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYI	Seryl-trna synthetase	1.83e+01
36 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYJ</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYJ</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYJ</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYJ	Seryl-trna synthetase	1.83e+01
37 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYK</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYK</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYK</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYK	Seryl-trna synthetase	1.83e+01
38 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYL</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYL</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYL</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYL	Seryl-trna synthetase	1.83e+01
39 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYM</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYM</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYM</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYM	Seryl-trna synthetase	1.83e+01
40 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYN</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYN</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYN</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYN	Seryl-trna synthetase	1.83e+01
41 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYO</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYO</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYO</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYO	Seryl-trna synthetase	1.83e+01
42 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYP</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYP</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYP</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYP	Seryl-trna synthetase	1.83e+01
43 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYQ</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYQ</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYQ</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYQ	Seryl-trna synthetase	1.83e+01
44 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYR</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYR</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYR</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYR	Seryl-trna synthetase	1.83e+01
45 <td>54</td> <td>64.3<td>421<td>5</td><td>ISRYS</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td></td>	54	64.3 <td>421<td>5</td><td>ISRYS</td><td>Seryl-trna synthetase</td><th>1.83e+01</th></td>	421 <td>5</td> <td>ISRYS</td> <td>Seryl-trna synthetase</td> <th>1.83e+01</th>	5	ISRYS	Seryl-trna synthetase	1.83e+01

ALIGNMENTS

RESULT	1	12WG	#type complete
ENTRY	1	parathyroid hormone 4	37 mutant N-TERMINAL SUCCINYLATED -
TITLE	1	synthetic	
ALTERNATE_NAMES		n-succinyl-hp(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		TN003319	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loessung,	
COMMENT		pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	
KEYWORDS		Resolution: not applicable	
FEATURE		disease mutation; hormone; signal	
2-9			
15-25			
SUMMARY		#region helix (right hand alpha)\	
		#region helix (right hand alpha)	
		length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 84; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 4.83e-05;	
Matches		11; Conservative 0; Mismatches 0; Gaps 0;	
DB	21	LRRKLDVHNF 31	
QY	1	LRRKLDVHNF 11	
RESULT	2	12WF	#type complete
ENTRY		parathyroid hormone 4	37 mutant N-TERMINAL ACETYLATED -
TITLE		synthetic	
ALTERNATE_NAMES		n-acetyl-hp(4-37)	
PDB_TITLE		structure of n-terminal acetylated human parathyroid hormone,	
ORGANISM		NMR, 10 structures	
REFERENCE		formal_name synthetic	
A67742			
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WF	
REFERENCE		TN003318	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loessung,	

PP.0, Bayreuth : University of Bayreuth (Thesis), 1996
 COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 3-6 #region helix (right hand alpha)\
 14-27 #region helix (right hand alpha)
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 84; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.83e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LRRKLDVHNF 31
 |||||
 QY 1 LRRKLDVHNF 11

Search completed: Thu Jul 30 11:10:03 1998
 Job time : 30 secs.

[W][O][R][L][D]

(TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:07:53 1998; Maspar time 2.18 seconds
Tabular output not generated. 126,596 Million cell updates/sec

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRRKLDVHNF 11

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 26.284; Variance 32.770; scale 0.802

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	84	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	9.02e-07
2	84	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	9.02e-07
3	84	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	9.02e-07
4	84	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	9.02e-07
5	84	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	9.02e-07
6	60	71.4	144	1	CITR_KLEPN CITRATE-PROTON SYMPORT	2.85e-01
7	57	67.9	184	1	GIG2_ARATH GLUCOSE-1-PHOSPHATE AD	1.17e+00
8	55	65.5	119	1	PTHY_CHICK PARATHYROID HORMONE PR	2.91e+00
9	55	65.5	162	1	Y4XD_RHNS HYPOTHEICAL 18.0 KD P	2.91e+00
10	55	65.5	305	1	HLYE_ECOLI HEMOLYSIN E (HEMOLYSIN	2.91e+00
11	55	65.5	462	1	COGK_MOUSE MACROPHAGE METALLOELAS	2.91e+00
12	54	64.3	189	1	YNOO_YEAST VERY HYPOTHEICAL 21.7	4.56e+00
13	54	64.3	233	1	DP3E_BUCAP DNA POLYMERASE III, EP	4.56e+00
14	54	64.3	421	1	SYS_THETH SERYL-TRNA SYNTHETASE	4.56e+00
15	54	64.3	752	1	HPRI_YEAST HPRI PROTEIN.	4.56e+00
16	53	63.1	102	1	YMB8_YEAST VERY HYPOTHEICAL 11.8	7.08e+00
17	53	63.1	227	1	PRRA_RAT PLACENTAL PROLACTIN-LI	7.08e+00
18	53	63.1	348	1	HMTI_YEAST HNRP ARGININE N-METHY	7.08e+00
19	53	63.1	500	1	CILA_HAEIN CITRATE LYASE ALPHA CH	7.08e+00
20	53	63.1	569	1	Y397_MYCPN HYPOTHEICAL PROTEIN M	1.09e+00
21	52	61.9	571	1	UREI_STAXY UREASE ALPHA SUBUNIT (1.09e+00
22	52	61.9	621	1	Y04E_MYCTU HYPOTHEICAL 69.2 KD P	1.09e+00
23	52	61.9	879	1	MYSP_DROME PARAYOSIN, LONG FORM.	1.09e+00

RESULT	ID	PTHY_BOVIN	STANDARD:	PRT:	115 AA.	ALIGNMENTS
AC	24	51	60.7	111	1	ARPP_BOVIN CAMP-REGULATED PHOSPHO
AC	25	51	60.7	133	1	YIMS_BPHI HYPOTHEICAL IMMUNITY
DT	26	51	60.7	310	1	SYNR_ARATH SYNAXIN-RELATED PROTE
DT	27	51	60.7	317	1	MSHR_BOVIN MELANOCYTE STIMULATING
DT	28	51	60.7	360	1	HIS8_LACIA HISTIDINOL-PHOSPHATE A
DT	29	51	60.7	419	1	MYC1_XENIA MYC 1 PROTO-ONCOGENE P
DT	30	51	60.7	431	1	CITL_ECOLI CITRATE-PROTON SYMPORT
DT	31	51	60.7	1444	1	CITL_SALTY CITRATE-PROTON SYMPORT
DT	32	51	60.7	1434	1	RNPL_RDV RNA-DIRECTED RNA POLYM
DT	33	51	60.7	2843	1	APC_HUMAN ADEMONATOUS POLYPOSIS
DT	34	50	59.5	281	1	P2C1_YEAST PROTEIN PHOSPHATASE 2C
DT	35	50	59.5	437	1	FOIC_HAEIN FOXYLPOLYGLUTAMATE SYN
DT	36	50	59.5	510	1	CITA_ECOLI CITRATE LYASE ALPHA CH
DT	37	50	59.5	525	1	Y107_METUA HYPOTHEICAL PROTEIN M
DT	38	50	59.5	586	1	YM61_CAEEL LEUKOTRIENE A-4 HYDROL
DT	39	50	59.5	609	1	LKHA_RAT LEUKOTRIENE A-4 HYDROL
DT	40	50	59.5	610	1	LKHA_MOUSE LEUKOTRIENE A-4 HYDROL
DT	41	50	59.5	610	1	LKHA_HUMAN RETINOBLASTOMA BINDING
DT	42	50	59.5	1257	1	RBB1_HUMAN SERINE/THROMBIN PROTE
DT	43	50	59.5	1314	1	SS22_YEAST DYNEIN HEAVY CHAIN, CY
DT	44	50	59.5	4725	1	DYHC_DICDI HYPOTHEICAL 48.8 KD P
DT	45	49	58.3	455	1	YHCL_ECOLI
DT	21-JUL-1986	(REL. 01, CREATED)				
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DT	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	BOS TAURUS (BOVINE).					
OS	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:					
OC	EUTHERIA: ARTIODACTYLA.					
OC	[1]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE: 80056617.					
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,					
RA	POTTS J.T., JR., RICH A.J.					
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).					
RL	[2]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE: 82037785.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).					
RL	[3]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE: 83105964.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).					
RL	[4]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE: 84262483.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RL	GENE 28:319-329(1984).					
RL	[5]					
RP	SEQUENCE OF 26-115.					
RA	MEDLINE: 74142666.					
RA	HAMILTON J.W., NATALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,					
RL	COHN D.V.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).					
RL	[6]					
RP	SEQUENCE OF 32-115.					
RA	MEDLINE: 71076162.					
RA	NATALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,					
RA	AURBACH G.D., POTTS J.T. JR.;					
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).					
RL	[7]					
RP	SEQUENCE OF 32-115.					
RA	MEDLINE: 71063634.					

Search completed: Thu Jul 30 11:08:00 1998
Job time : 7 secs.

RA BREWER H.B. JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIAL H.D., SAUER R.,
RA DEFLOS L.J., DAMSON B.F., HOGAN M.L., AUBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: J000106; G85; -;
DR EMBL: J00023; G163641; -;
DR EMBL: J00024; G163643; -;
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: K01938; G163647; -;
DR EMBL: M25082; G163645; -;
DR PIR: A01534; PTRO
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
RN [1]
RA HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match
Best Local Similarity 100.0%; Score 84; DB 1; Length 115;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LRRKLDVHNF 65
QY 1 LRRKLDVHNF 11

RESULT 2
ID ID PTHY-CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANT'S PAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
RN [1]
RA SEQUENCE FROM N.A.
RA TISSUE-PARATHYROID;
RA MEDLINE: 95369696.
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
RA DENTLE J.W., CAPEN C.C.;
RL GENE 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: U15662; G558916; -;
DR PROSITE: PS00335; PARATHYROID; 1.
DR HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;

Query Match
Best Local Similarity 100.0%; Score 84; DB 1; Length 115;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LRRKLDVHNF 65
QY 1 LRRKLDVHNF 11

MIRCH

(TW)

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MIRCH.p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:08:17 1998; Maspar time 3.90 Seconds
118.655 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRRKLDVHNF 11

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: stremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 25.128; Variance 32.322; scale 0.777

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	74	88.1	105	10	PARATHYROID HORMONE (F	2.88e-04
2	59	70.2	2475	11	POLYPROTEIN PP220.	5.64e-01
3	58	69.0	591	3	F52E10.5 (FRAGMENT).	9.04e-01
4	57	67.9	299	3	SIMILAR TO SER/THR PRO	1.44e+00
5	57	67.9	320	9	HYPOTHETICAL PROTEIN I	1.44e+00
6	56	66.7	1291	2	MRNA (K1AA0067) FOR OR	2.28e+00
7	55	65.5	453	1	HYPOTHETICAL 50.0 KD P	3.60e+00
8	55	65.5	1459	3	R09E10.5	3.60e+00
9	55	65.5	2708	3	CHLOROQUINE RESISTANCE	3.60e+00
10	55	65.5	2742	3	CHLOROQUINE RESISTANCE	3.60e+00
11	55	65.5	2819	3	STRAIN HB3 CG2 (CG2).	5.65e+00
12	54	64.3	207	11	ORF36L.	5.65e+00
13	54	64.3	342	1	CHROMOSOME XII COSMID	5.65e+00
14	54	64.3	400	3	TEKTIN B1	5.65e+00
15	54	64.3	735	3	C06G3.9 PROTEIN.	5.65e+00
16	53	63.1	265	8	AGL15 TYPE 2.	8.80e+00
17	53	63.1	373	3	C04G6.2 PROTEIN.	8.80e+00
18	53	63.1	398	8	SIMILAR TO SACHAROMYC	8.80e+00
19	53	63.1	1744	3	T14G8.1 (FRAGMENT).	8.80e+00
20	52	61.9	90	3	COSMID F11611.	1.36e+01

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	063473	88.1	105	10	PARATHYROID HORMONE (F	2.88e-04	
2	063473	70.2	2475	11	POLYPROTEIN PP220.	5.64e-01	
3	063473	69.0	591	3	F52E10.5 (FRAGMENT).	9.04e-01	
4	063473	67.9	299	3	SIMILAR TO SER/THR PRO	1.44e+00	
5	063473	67.9	320	9	HYPOTHETICAL PROTEIN I	1.44e+00	
6	063473	66.7	1291	2	MRNA (K1AA0067) FOR OR	2.28e+00	
7	063473	65.5	453	1	HYPOTHETICAL 50.0 KD P	3.60e+00	
8	063473	65.5	1459	3	R09E10.5	3.60e+00	
9	063473	65.5	2708	3	CHLOROQUINE RESISTANCE	3.60e+00	
10	063473	65.5	2742	3	CHLOROQUINE RESISTANCE	3.60e+00	
11	063473	65.5	2819	3	STRAIN HB3 CG2 (CG2).	5.65e+00	
12	063473	64.3	207	11	ORF36L.	5.65e+00	
13	063473	64.3	342	1	CHROMOSOME XII COSMID	5.65e+00	
14	063473	64.3	400	3	TEKTIN B1	5.65e+00	
15	063473	64.3	735	3	C06G3.9 PROTEIN.	5.65e+00	
16	063473	63.1	265	8	AGL15 TYPE 2.	8.80e+00	
17	063473	63.1	373	3	C04G6.2 PROTEIN.	8.80e+00	
18	063473	63.1	398	8	SIMILAR TO SACHAROMYC	8.80e+00	
19	063473	63.1	1744	3	T14G8.1 (FRAGMENT).	8.80e+00	
20	063473	61.9	90	3	COSMID F11611.	1.36e+01	

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	063473	88.1	105	10	PARATHYROID HORMONE (F	2.88e-04	
2	063473	70.2	2475	11	POLYPROTEIN PP220.	5.64e-01	
3	063473	69.0	591	3	F52E10.5 (FRAGMENT).	9.04e-01	
4	063473	67.9	299	3	SIMILAR TO SER/THR PRO	1.44e+00	
5	063473	67.9	320	9	HYPOTHETICAL PROTEIN I	1.44e+00	
6	063473	66.7	1291	2	MRNA (K1AA0067) FOR OR	2.28e+00	
7	063473	65.5	453	1	HYPOTHETICAL 50.0 KD P	3.60e+00	
8	063473	65.5	1459	3	R09E10.5	3.60e+00	
9	063473	65.5	2708	3	CHLOROQUINE RESISTANCE	3.60e+00	
10	063473	65.5	2742	3	CHLOROQUINE RESISTANCE	3.60e+00	
11	063473	65.5	2819	3	STRAIN HB3 CG2 (CG2).	5.65e+00	
12	063473	64.3	207	11	ORF36L.	5.65e+00	
13	063473	64.3	342	1	CHROMOSOME XII COSMID	5.65e+00	
14	063473	64.3	400	3	TEKTIN B1	5.65e+00	
15	063473	64.3	735	3	C06G3.9 PROTEIN.	5.65e+00	
16	063473	63.1	265	8	AGL15 TYPE 2.	8.80e+00	
17	063473	63.1	373	3	C04G6.2 PROTEIN.	8.80e+00	
18	063473	63.1	398	8	SIMILAR TO SACHAROMYC	8.80e+00	
19	063473	63.1	1744	3	T14G8.1 (FRAGMENT).	8.80e+00	
20	063473	61.9	90	3	COSMID F11611.	1.36e+01	

RN [2]
RP COMPLETE GENOME.
RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA RODRIGUEZ J.F., VINUELA E.,
RL VIROLOGY 208:249-278(1995).
CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
CC PROTEINS P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.
DR EMBL; Z22777; G394709; -.
DR EMBL; U18466; G780461; -.
KM POLYPROTEIN.
SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3C0A CRC32;

Query Match 70.2%; Score 59; DB 11; Length 2475;
Best Local Similarity 72.7%; Pred. No. 5.64e-01;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1944 LRKTLQDVISF 1954
||| ||| :|
QY 1 LRKTLQDVHNF 11

Search completed: Thu Jul 30 11:09:14 1998
Job time : 57 secs.

MIRAGE
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:12:42 1998; MasPar time 2.67 Seconds
57.535 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-31
Description: (1-10) from US08817547A.pep
Perfect Score: 73
Sequence: 1 LRRK1QDVHN 10

Scoring table:
PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 17.167; Variance 59.785; scale 0.287

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	73	100.0	33 18	R88841	Human parathyroid hor	8.53e-01
2	73	100.0	34 26	R62432	Accelerator peptide b	8.53e-01
3	73	100.0	34 9	R45508	Parathyroid hormone/p	8.53e-01
4	73	100.0	34 9	R45528	Parathyroid hormone/p	8.53e-01
5	73	100.0	34 13	R69037	PTH analogue with amp	8.53e-01
6	73	100.0	34 7	R34353	Human parathyroid hor	8.53e-01
7	73	100.0	34 7	R34352	Bovine parathyroid ho	8.53e-01
8	73	100.0	34 7	R34345	Bovine parathyroid ho	8.53e-01
9	73	100.0	34 8	R41582	[Arg15,16,17]hPTH (1-	8.53e-01
10	73	100.0	34 22	W20002	Cyclised rat parathyr	8.53e-01
11	73	100.0	34 22	W20003	Cyclised [Nle 8,18, T	8.53e-01
12	73	100.0	34 22	W17962	Human PTH analogue [C	8.53e-01
13	73	100.0	35 14	R74442	Parathyroid hormone p	8.53e-01
14	73	100.0	35 14	R74413	Parathyroid hormone p	8.53e-01
15	73	100.0	35 14	R74527	Human parathyroid hor	8.53e-01
16	73	100.0	36 9	R58243	Propargy1-[Al]-hPTH(1	8.53e-01
17	73	100.0	36 9	R58057	[L8, D10, A16, Q18]-hPTH	8.53e-01
18	73	100.0	36 9	R58026	N-alpha-methyl[Ala11]	8.53e-01
19	73	100.0	36 9	R58177	Morpholine-2-carboxy	8.53e-01

20	73	100.0	38 9	R58089	[Arg12]-hPTH(1-38)-OH	8.53e-01
21	73	100.0	38 9	R58061	[Ile13]-hPTH(1-38)-OH	8.53e-01
22	73	100.0	38 9	R58091	[Cys13]-hPTH(1-38)-OH	8.53e-01
23	73	100.0	38 9	R58028	[Thr1]-hPTH(1-38)-OH	8.53e-01
24	73	100.0	38 9	R58124	[Lys19]-hPTH(1-38)-OH	8.53e-01
25	73	100.0	44 26	P30015	Human parathyroid hor	8.53e-01
26	73	100.0	84 27	W25687	Human parathyroid hor	8.53e-01
27	73	100.0	84 4	R21244	Human parathyroid hor	8.53e-01
28	73	100.0	84 4	R23453	Bovine parathyroid ho	8.53e-01
29	73	100.0	84 4	R23453	Porcine parathyroid h	8.53e-01
30	73	100.0	84 4	R23242	Human parathyroid hor	8.53e-01
31	73	100.0	84 4	R23241	Human parathyroid hor	8.53e-01
32	73	100.0	84 4	R23346	Bovine parathyroid ho	8.53e-01
33	73	100.0	84 4	R23336	Bovine parathyroid ho	8.53e-01
34	73	100.0	84 4	R23529	Human parathyroid hor	8.53e-01
35	73	100.0	84 4	R21217	Human parathyroid hor	8.53e-01
36	73	100.0	84 4	R21198	Human parathyroid hor	8.53e-01
37	73	100.0	84 4	R23251	Bovine parathyroid hor	8.53e-01
38	73	100.0	84 4	R21256	Human parathyroid hor	8.53e-01
39	73	100.0	84 4	R23368	Bovine parathyroid ho	8.53e-01
40	73	100.0	84 6	R30857	Leu18 hPTH mutein.	8.53e-01
41	73	100.0	84 6	R30856	Cys35 hPTH mutein.	8.53e-01
42	73	100.0	84 4	R21241	Human parathyroid hor	8.53e-01
43	73	100.0	84 4	R21240	Human parathyroid hor	8.53e-01
44	73	100.0	84 4	R23474	Porcine parathyroid h	8.53e-01
45	73	100.0	84 4	R23475	Porcine parathyroid h	8.53e-01

ALIGNMENTS

RESULT 1
ID R88841 standard; peptide; 33 AA.

AC R88841;
DT 07-OCT-1996 (first entry)
DE Human parathyroid hormone analogue, [Leu27]-hPTH(1-33)-NH2.
KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;
KW calcium regulation; reduced PKC activity; protein kinase C;
KW increased adenylyl cyclase activity; cAMPase; bone loss.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 33 /note="amdated"

PN CA2126299-A.
PD 21-DEC-1995.
PF 20-JUN-1994; 126299.
PR 20-JUN-1994; CA-126299.
PA (WILLI) WILLICK G E.
PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
PI Willick GB;
DR WPI: 96-151754/16.
PT New human parathyroid hormone analogues - which have increased
PT adenylyl cyclase activating activity, used for treating osteoporosis
PS Claim 2; Page -: 21pp; English.

CC R88829-R88841 are human parathyroid hormone (PTH) analogues. The
CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
CC activity and reduce protein kinase C (PKC) activity. The analogues
CC can reverse the loss of bone and increase bone mass and density
CC without undesirable effects. They are useful for the treatment of
CC osteoporosis and other bone related disorders and disorders
CC involving bone cell calcium regulation.
SQ Sequence 33 AA.

Query Match 100.0%; Score 73; DB 18; Length 33;
Best Local Similarity 100.0%; Pred. No. 8.53e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 Lrrk1Qdvhn 33
QY 1 LRRK1QDVHN 10

RESULT 2
ID R62432 standard; peptide; 34 AA.

AC R62432: (first entry)
 DT 31-JUL-1995
 DE Accelerator peptide basic region peptide, p-8.
 KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
 KW periodontal tissue; regeneration; periodontitis; periodontal pocket;
 KW down growth; epithelium; fibre adhesion; cement.
 OS Synthetic.
 PN J06234653-A.
 PD 23-AUG-1994.
 PF 10-FEB-1993; 045998.
 PR 10-FEB-1993; JP-045998.
 PA (SUNZ) SUNSTAR CHEM IND CO LTD.
 DR WPI; 95-157631/21.
 PT Accelerator for regenerating periodontal tissue - comprises
 PT peptide having 3-34 aminoacid residues having connected basic
 PT aminoacid residues
 PS Disclosure; page 3; 7pp; Japanese.
 CC The sequences in R62425-36 are peptide fragments of an accelerator
 CC protein which contain at least two basic amino acids. The accelerator
 CC also comprises a cell growth factor. The accelerator may be used to
 CC accelerate the growth of periodontal tissue regeneration. The
 CC accelerator is applied by opening the gingiva, treating the tissue
 CC destroyed by periodontitis and applying the accelerator in the
 CC periodontal pocket. The accelerator reduces the down growth of the
 CC epithelium and accelerates fibre adhesion and regenerates cement.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 73; DB 26; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8.33e-01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 24 LKKKIQDVHN 33
 |||||
 QY 1 LRRKLDVHN 10

Search completed: Thu Jul 30 11:13:00 1998
 Job time : 18 secs.

COMMENT PP, 0, Bayreuth : University of Bayreuth (Thesis), 1996
 COMMENT Resolution: not applicable
 KEYWORDS Determination: NMR
 FEATURE disease mutation; hormone; signal
 3-6
 14-27
 SUMMARY #region helix (right hand alpha) \
 #region helix (right hand alpha) \
 #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 73; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.82e-03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 21 LRRKLQDVHN 30
 |||||||||
 Oy 1 LRRKLQDVHN 10

Search completed: Thu Jul 30 11:12:24 1998
 Db time : 17 secs.

Thu Jul 30 13:38:13 1998

 Maspar time 2.16 Seconds
 116.179 Million cell updates/sec

 Maspar time 2.16 Seconds
 116.179 Million cell updates/sec

 Maspar time 2.16 Seconds
 116.179 Million cell updates/sec

 Maspar time 2.16 Seconds
 116.179 Million cell updates/sec

 Maspar time 2.16 Seconds
 116.179 Million cell updates/sec

 Maspar time 2.16 Seconds
 116.179 Million cell updates/sec

 Maspar time 2.16 Seconds
 116.179 Million cell updates/sec

SUMMARIES

Build No.	Score	Query Match	Length	ID	Description	Pred. No.
1	73	100.0	115	1	PTHY_BOVIN	8.74e-05
2	73	100.0	115	1	PTHY_CANFA	8.74e-05
3	73	100.0	115	1	PTHY_PIG	8.74e-05
4	73	100.0	115	1	PTHY_RAT	8.74e-05
5	73	100.0	115	1	PTHY_HUMAN	8.74e-05
6	53	75.3	119	1	PTHY_CHICK	1.06e+00
7	54	74.0	121	1	PTHY_CHICK	1.06e+00
8	53	72.6	349	1	HMT1_YEAST	2.72e+00
9	53	71.2	621	1	Y397_MYCPN	4.31e+00
10	52	71.2	879	1	Y397_MYCPN	4.31e+00
11	52	71.2	879	1	Y397_MYCPN	4.31e+00
12	51	69.9	310	1	MSHR_BOVIN	6.80e+00
13	51	69.9	317	1	MSHR_BOVIN	6.80e+00
14	51	69.9	317	1	MSHR_BOVIN	6.80e+00
15	50	68.5	360	1	HIS8_LACIA	1.07e+01
16	50	68.5	437	1	HIS8_LACIA	1.07e+01
17	50	68.5	586	1	YMG1_CAEEL	1.07e+01
18	50	68.5	586	1	YMG1_CAEEL	1.07e+01
19	49	67.1	209	1	DIHC_DICDI	1.66e+01
20	49	67.1	444	1	CITR1_KLEPN	1.66e+01
21	49	67.1	444	1	CITR1_KLEPN	1.66e+01
22	48	65.8	154	1	Y17K_SSV1	2.56e+01
23	48	65.8	229	1	YADJ_BACSD	2.56e+01

RESULT	ID	PTHY_BOVIN	STANDARD	PRT	115 AA.
AC	P01268				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; ARTIODACTYLA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 80056617.				
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOU B.J.A., NATHANS J., SHARP P.A.,				
RA	POTTS J.T. JR., RICH A.;				
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 82037785.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;				
RL	GENE 28:319-329(1984).				
RN	[5]				
RP	SEQUENCE OF 26-115.				
RX	MEDLINE; 74142666.				
RA	HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,				
RA	COHN D.V.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).				
RN	[6]				
RP	SEQUENCE OF 32-115.				
RX	MEDLINE; 71076162.				
RA	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,				
RA	AUBACH G.D., POTTS J.T. JR.;				
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).				
RN	[7]				
RP	SEQUENCE OF 32-115.				
RX	MEDLINE; 71063634.				

US-08-817-547A-31.rsp

Page 2

RITTY.
 "TY.
 "ORMONE.
 "2;
 "length 115;
 "ndels 0,
 Caps 0

W I S E N H (TM)

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 09:57:51 1998; MasPar time 6.04 Seconds
Molecular output not generated. 25.396 Million cell updates/sec

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68
Sequence: 1 SVSEIQLMHN 10

Scoring table:
PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.093; Variance 66.058; scale 0.244

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	68	100.0	34 22	W17954	Human parathyroid hor	6.37e+00
2	68	100.0	34 22	W17955	Human parathyroid hor	6.37e+00
3	68	100.0	34 22	W17950	Human PTH analogue [C	6.37e+00
4	68	100.0	34 22	W20006	Cyclised human parath	6.37e+00
5	68	100.0	34 7	R34366	Human parathyroid hor	6.37e+00
6	68	100.0	34 7	R34362	Human parathyroid hor	6.37e+00
7	68	100.0	34 20	W14310	Cyclic parathyroid ho	6.37e+00
8	68	100.0	34 20	W14309	Cyclic parathyroid ho	6.37e+00
9	68	100.0	34 22	W17947	Human parathyroid hor	6.37e+00
10	68	100.0	34 7	R34365	Human parathyroid hor	6.37e+00
11	68	100.0	34 7	R34364	Human parathyroid hor	6.37e+00
12	68	100.0	34 7	R34356	Human parathyroid hor	6.37e+00
13	68	100.0	34 9	R58228	(D-Asp30)-hPTH(1-34)-	6.37e+00
14	68	100.0	36 9	R58301	(NMeVal36)-hPTH(1-36)	6.37e+00
15	68	100.0	36 9	R58298	(NMeVal35)-hPTH(1-36)	6.37e+00
16	68	100.0	36 9	R58276	(Met(O2)181)-hPTH(1-36)	6.37e+00
17	68	100.0	36 9	R58275	(Ala16)-hPTH(1-36)-NH	6.37e+00
18	68	100.0	36 9	R58242	[Lys(Iso)prolyl]131-hP	6.37e+00
19	68	100.0	36 9	R58191	[Ala54]-hPTH(1-36)-NH	6.37e+00

20	68	100.0	36 9	R58278	[D-Met18]-hPTH(1-36)-	6.37e+00
21	68	100.0	36 9	R58289	[Ala25]-hPTH(1-36)-NH	6.37e+00
22	68	100.0	36 9	R58290	[Ala26]-hPTH(1-36)-NH	6.37e+00
23	68	100.0	36 9	R58284	[D-Trp23]-hPTH(1-36)-	6.37e+00
24	68	100.0	36 9	R58260	[D-Val2]-hPTH(1-36)-N	6.37e+00
25	68	100.0	36 9	R58264	[D-Gln6]-hPTH(1-36)-N	6.37e+00
26	68	100.0	36 9	R58198	[D-Ser3]-hPTH(1-36)-N	6.37e+00
27	68	100.0	36 9	R58234	[Ala32]-hPTH(1-36)-NH	6.37e+00
28	68	100.0	36 9	R58287	[Phe25]-hPTH(1-36)-NH	6.37e+00
29	68	100.0	36 9	R58288	[Lys25]-hPTH(1-36)-NH	6.37e+00
30	68	100.0	36 9	R58249	[D-Ser1]-hPTH(1-36)-N	6.37e+00
31	68	100.0	36 8	R39450	Ser-Val(hPTH 3-35)-P	6.37e+00
32	68	100.0	36 9	R58274	[Ala15]-hPTH(1-36)-NH	6.37e+00
33	68	100.0	37 9	R58244	[Ala0]-hPTH(1-36)-NH2	6.37e+00
34	68	100.0	37 5	R24778	hPTH(1-37)-amide/ethy	6.37e+00
35	68	100.0	38 9	R58131	[Gly19]-hPTH(1-38)-OH	6.37e+00
36	68	100.0	38 9	R58105	[Val14]-hPTH(1-38)-OH	6.37e+00
37	68	100.0	38 9	R58077	[Leu33]-hPTH(1-38)-OH	6.37e+00
38	68	100.0	38 9	R58097	[Thr13]-hPTH(1-38)-OH	6.37e+00
39	68	100.0	38 9	R58109	[Thr14]-hPTH(1-38)-OH	6.37e+00
40	68	100.0	44 26	P30015	Human parathyroid hor	6.37e+00
41	68	100.0	47 25	W21946	Human parathyroid hor	6.37e+00
42	68	100.0	84 27	W25687	Fusion protein compri	6.37e+00
43	68	100.0	84 25	W29420	Human parathyroid hor	6.37e+00
44	68	100.0	84 4	R23790	Human parathyroid hor	6.37e+00
45	68	100.0	229 9	R47971	Parathyroid hormone g	6.37e+00
					Sequence of a full-le	

ALIGNMENTS

RESULT 1	W17954 standard; peptide; 34 AA.
ID	W17954;
AC	29-JUL-1997 (first entry)
DT	Human parathyroid hormone analogue [Alb19]hPTH(1-34)NH2.
DE	Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW	bone fracture.
OS	Homo sapiens.
FS	Synthetic.
FT	Key
FT	modified_site 19 location/Qualifiers
FT	modified_site 34 /label= Alb
FT	modified_site 34 /note= "In amide form"
FN	WO9702834-A1.
PD	30-JAN-1997.
PD	03-JUL-1996; U11292.
PR	13-JUL-1995; US-001105.
PR	06-SEP-1995; US-003305.
PR	29-MAR-1996; US-626186.
PA	(BIOM-) BIOMASURE INC.
PI	Dong zx;
DR	WPI; 97-118819/11.
PT	New variants of human parathyroid hormone 1-34 peptide - which
PT	stimulate bone growth and are used for treatment of osteoporosis and
PT	bone fracture
PS	Claim 11; Page -; 33pp; English.
CC	The present sequence is a specific example of a human parathyroid
CC	hormone (hPTH) analogue from fragment 1-34 in which at least one
CC	of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
CC	is alpha-aminoisobutyric acid (Aib). In this example the glu residue
CC	at position 19 of the wild-type has been substituted by Aib. The hPTH
CC	analogues stimulate bone growth and so are useful in human or veterinary
CC	medicine for treatment of osteoporosis and bone fracture, optionally in
CC	conjunction with anti-resorptive therapy (bisphosphonates and
CC	calcitonin).
CC	N.B. The present sequence does not appear in the specification. It
CC	corresponds to the known hPTH 1-34 fragment with the modifications
CC	as stated in the claim.
SQ	Sequence 34 AA.
Query Match	100.0%; Score 68; DB 22; Length 34;
Best Local Similarity	100.0%; Pred. No. 6.37e+00;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 svseiqimhn 10
 |||||
 QY 1 SVSEIQIMHN 10

RESULT 2
 ID W17955 standard: peptide; 34 AA.

AC W17955;
 DT 29-JUL-1997 (first entry)
 DE Human parathyroid hormone analogue [Alb34]hPTH(1-34)NH2.
 KM Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 KM bone fracture.
 OS Homo sapiens.
 OS Synthetic.
 FH key Location/Qualifiers
 FT modified_site 34
 /label= Alb
 /note= "in amide form"

PD WO9702834-A1.
 30-JAN-1997
 PF 03-JUL-1996; U11292
 PR 13-JUL-1995; US-001105.
 PR 06-SEP-1995; US-003305.
 PR 29-MAR-1996; US-626186.
 PA (BIOM-) BIOMEASURE INC.
 PI Dong ZX;
 DR WPI; 97-118819/11.
 PT New variants of human parathyroid hormone 1-34 peptide - which
 PT stimulate bone growth and are used for treatment of osteoporosis and
 PT bone fracture
 PS Claim 11: Page -: 33pp; English.
 CC The present sequence is a specific example of a human parathyroid
 CC hormone (hPTH) analogue from fragment 1-34 in which at least one
 CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
 CC is alpha-aminoisobutyric acid (Aib). In this example the phe residue
 CC at position 34 of the wild-type has been substituted by Aib. The hPTH
 CC analogues stimulate bone growth and so are useful in human or veterinary
 CC medicine for treatment of osteoporosis and bone fracture, optionally in
 CC conjunction with anti-resorptive therapy (bisphosphonates and
 CC calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 CC corresponds to the known hPTH 1-34 fragment with the modifications
 CC as stated in the claim.
 SO Sequence 34 AA;

Query Match 100.0%; Score 68; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred.No. 6.37e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 svseiqimhn 10
 |||||
 QY 1 SVSEIQIMHN 10

Search completed: Thu Jul 30 09:58:02 1998
 Job time : 11 secs.

NWSEKJ
***** (TW)

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MSrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 09:57:07 1998; MasPar time 3.27 Seconds
111.690 Million cell updates/sec
Molecular output not generated.

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68
Sequence: 1 SVSEIQLMHN 10

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 3653193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 22.419; Variance 28.455; scale 0.788

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	68	100.0	34	5	12WA parathyroid hormone (4.43e-04	
2	68	100.0	37	5	1HPH parathyroid hormone f 4.43e-04	
3	68	100.0	115	1	PTHU parathyroid hormone p 4.43e-04	
4	68	100.0	115	1	PRPG parathyroid hormone p 4.43e-04	
5	66	97.1	115	1	AO5091 parathyroid hormone p 1.32e-03	
6	64	94.1	36	5	12WB parathyroid hormone (3.87e-03	
7	64	94.1	105	2	151851 parathyroid hormone (3.87e-03	
8	63	92.6	119	2	A34937 parathyroid hormone - 6.60e-03	
9	61	89.7	115	2	JC4202 parathyroid hormone - 1.89e-02	
10	59	86.8	37	5	12WC parathyroid hormone (5.34e-02	
11	59	86.8	115	1	PTBO parathyroid hormone (5.34e-02	
12	57	83.8	34	5	12WD cyclic parathyroid ho 1.48e-01	
13	57	83.8	35	5	12WE parathyroid hormone (1.48e-01	
14	53	77.9	34	5	12WE parathyroid hormone (1.07e+00	
15	53	77.9	34	5	12WG parathyroid hormone 4 1.07e+00	
16	53	77.9	34	5	12WF parathyroid hormone 4 1.07e+00	
17	50	73.5	383	2	B42377 acetylornithine deace 4.47e+00	
18	48	70.6	448	2	S76701 hypothetical protein 1.12e+01	
19	48	70.6	1015	2	S55474 human giant larvae ho 1.12e+01	
20	47	69.1	108	2	S23204 retinol-binding prote 1.77e+01	
21	47	69.1	176	2	S27192 retinol-binding prote 1.77e+01	
22	46	67.6	445	2	B40970 undulin 2 - human (fr 2.76e+01	
23	46	67.6	843	2	A40970 undulin 1 - human (fr 2.76e+01	

ENTRY	1	12WA	#type complete
24	46	67.6	1034
25	46	67.6	1371
26	46	67.6	2163
27	45	66.2	152
28	45	66.2	175
29	45	66.2	176
30	45	66.2	177
31	45	66.2	177
32	45	66.2	177
33	45	66.2	209
34	45	66.2	324
35	45	66.2	393
36	45	66.2	405
37	45	66.2	444
38	45	66.2	494
39	44	64.7	338
40	44	64.7	490
41	44	64.7	508
42	44	64.7	542
43	44	64.7	553
44	44	64.7	557
45	44	64.7	610

ALIGNMENTS

ENTRY	1	12WA	#type complete
24	46	67.6	1034
25	46	67.6	1371
26	46	67.6	2163
27	45	66.2	152
28	45	66.2	175
29	45	66.2	176
30	45	66.2	177
31	45	66.2	177
32	45	66.2	177
33	45	66.2	209
34	45	66.2	324
35	45	66.2	393
36	45	66.2	405
37	45	66.2	444
38	45	66.2	494
39	44	64.7	338
40	44	64.7	490
41	44	64.7	508
42	44	64.7	542
43	44	64.7	553
44	44	64.7	557
45	44	64.7	610

RESULT 1
ENTRY 1
TITLE 12WA
ALTERNATE_NAMES parathyroid hormone (residues 1-34) - human
PDB_TITLE HPTH(1-34)
PDB_AUTHOR structure of human parathyroid hormone fragment 1-34, NMR 10 structures
ORGANISM #formal_name Homo sapiens #common_name man
REFERENCE A67856
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WA
REFERENCE TN001717
#authors Marx, U.C.
#book In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS hormone
FEATURE 6-9
#region helix (right hand alpha)\
SUMMARY 19-30
#region helix (right hand alpha)\
#length 34 #molecular-weight 4118 #checksum 5629
Query Match 100.0%; Score 68; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.43e-04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 SVSEIQLMHN 10
QY 1 SVSEIQLMHN 10
RESULT 2
ENTRY 1HPH
TITLE parathyroid hormone fragment 1 37 (hpth(1-37)) (NMR, 10 structures) - synthetic
ORGANISM #formal_name synthetic
REFERENCE A65802
#authors Marx, U.C.; Roesch, P.
#submission submitted to the Brookhaven Protein Data Bank, February 1995
#cross-references PDB:1HPH
COMMENT Resolution: not applicable
COMMENT Determination: NMR
COMMENT R-value: no refinement
KEYWORDS hormone
FEATURE 6-9
#region helix (right hand alpha)\

US-08-817-547A-1.RPI

Thu Jul 30 13:37:52 1998

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17-28      #region helix (right hand alpha) #checksum 3791
SUMMARY      #length 37 #molecular-weight 4401
Query Match 100.0%; Score 68; DB 5; length 37;
Best Local Similarity 100.0%; Pred. No. 4.43e-04; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
Db 1 SVSEIOLMHN 10
QY 1 SVSEIOLMHN 10

Search completed: Thu Jul 30 09:57:31 1998
Job time : 24 secs.

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MUSE (TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 09:55:44 1998; Maspar time 2.16 Seconds
ular output not generated. 116.271 Million cell updates/sec

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68
Sequence: 1 SVSEIQLMHN 10

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.348; Variance 23.508; scale 0.993

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	68	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	9.25e-06
2	68	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	9.25e-06
3	66	97.1	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.53e-05
4	63	92.6	119	1	PTHY_CHICK PARATHYROID HORMONE PR	2.53e-04
5	61	89.7	115	1	PTHY_CANFA PARATHYROID HORMONE PR	9.17e-04
6	59	86.8	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	3.25e-03
7	50	73.5	369	1	PROB_CORGL GLUTAMATE 5-KINASE (EC	6.99e-01
8	50	73.5	383	1	ARGE_ECOLI ACETYLORNITHINE DEACT	3.65e+00
9	47	69.1	176	1	RETI_ONCMV PLASMA RETINOL-BINDING	3.65e+00
10	47	69.1	176	1	RETI_ONCMV PLASMA RETINOL-BINDING	3.65e+00
11	47	69.1	435	1	Y413_ARATH HYPOTHETICAL 48.8 KD P	3.65e+00
12	46	67.6	2163	1	BRR2_YEAST PRE-MRNA SPLICING HELI	6.23e+00
13	45	66.2	175	1	PTHY_MOUSE PARATHYROID HORMONE-RE	1.05e+01
14	45	66.2	176	1	PTHY_CHICK PARATHYROID HORMONE-RE	1.05e+01
15	45	66.2	177	1	PTHY_RAT PARATHYROID HORMONE-RE	1.05e+01
16	45	66.2	177	1	PTHY_CANFA PARATHYROID HORMONE-RE	1.05e+01
17	45	66.2	177	1	PTHY_HUMAN PARATHYROID HORMONE-RE	1.05e+01
18	45	66.2	324	1	IG_GAMMA-1 CHAIN C REG	1.05e+01
19	45	66.2	393	1	GC1_MOUSE IG GAMA-1 CHAIN C REG	1.05e+01
20	45	66.2	494	1	PR31_YEAST PRE-MRNA SPLICING FACT	1.05e+01
21	44	64.7	151	1	LE14_GOSHI LATE EMBRYOGENESIS ABU	1.76e+01
22	44	64.7	267	1	DHPS_SNAHA DIHYDROPTEROATE SYNTHA	1.76e+01
23	44	64.7	338	1	CYSP_SALTY THIOSULFATE-BINDING PR	1.76e+01

RESULT	ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	P01270;					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
CC	EUTHERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 82150870.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.;					
RA	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RX	MEDLINE; 74174967.					
RA	JACOBS J.W., KEMPER B., NITAL H.D., HABENER J.F., POTTS J.T. JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RX	MEDLINE; 74111656.					
RA	NITAL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;					
RA	O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RX	MEDLINE; 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;					
RA	POTTS J.T. JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NITAL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;					
RA	O'RIORDAN J.L.H., POTTS J.T. JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.;					
RL	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

REVOLUTIONS. 17416516.
RP MEDLINE: 75146516. NIALL H.D., O'RIOURAN J.L.H., POTTS J.T. JR.;
RA KEUTMANN H.T., 14:1842-1847(1975).
RA BIOCHEMISTRY 14:1842-1847(1975).
RL [8]
RP SYNTHESIS OF 32-65.
RP MEDLINE: 75059420. RIETSCHOTEN J., GREEN E., NIALL H.D., JR.;
RX TREEBEAR G.W., VAN PARSONS J.A., O'RIOURAN J.L.H., POTTS J.T. JR.;
RA KEUTMANN H.T., PHYSIOL. CHEM. 355:415-421(1974).
RA HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 355:415-421(1974).
RL [9]
RN SYNTHESIS OF 32-65.
RN MEDLINE: 73227467.
RX ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
RX ANDREATA R.H., RITTEL W., SIEBER P.,
RA RINKER B., RITTEL W., 47:40-43(1973).
RA HELV. CHIM. ACTA 56:470-473(1973).
RN [10]
RN STRUCTURE BY NMR OF 32-65.
RN MEDLINE: 91299748.
RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
RA BIOCHEMISTRY 30:6936-6942(1991).
RN [11]
RN STRUCTURE BY NMR OF 32-65.
RN MEDLINE: 93345518.
RA BARDEN J.A., CUTHBERTSON R.M.;
RA EUR. J. BIOCHEM. 215:315-321(1993).
RN [12]
RN STRUCTURE BY NMR OF 32-68.
RN MEDLINE: 95318084.
RX MARX U.C., AUSTERMANN S., BAYER P., ADELMANN K., ECHART A.,
RA STICHT H., WALTER S., SCHMID F.-X., JAEHNICK R., FORSMANN W.-G.,
RA ROESCH P.,
RA J. BIOL. CHEM. 270:15194-15202(1995).
RL [13]
RL VARIANT ARG-18.
RL MEDLINE: 91009811.
RA ARNOLD A., HORST S.A., GARDELIA T.J., BABA H., LEVINE M.A.,
RA KROEMER H.M., 86:1084-1087(1990).
RL J. CLIN. INVEST. PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
-1- FUNCTION: PTH PREVENTS THEIR RENAL EXCRETION.
CC BONE AND PREVENTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
CC -1- DISEASE: DEFECTS IN PTH.
CC HYPOPARATHYROIDISM (FTH).
CC EXHL: J00301; G150704; -
CC EXHL: V00597; G37144; -
CC EXHL: A29146; E186700; -
DR EXHL: A01536; PTHU.
DR PIR: A19339; A19338.
DR PIR: 1HPH: 10-JUL-85.
DR PDB: 1H7H: 15-OCT-87.
DR PDB: 1H7A: 12-MAR-97.
DR PDB: 1H7B: 12-MAR-97.
DR PDB: 1H7C: 12-MAR-97.
DR PDB: 1H7D: 12-MAR-97.
DR PDB: 1H7E: 12-MAR-97.
DR PDB: 1H7F: 16-JUN-97.
DR PDB: 1H7G: 16-JUN-97.
DR PDB: 1H7H: 16-JUN-97.
DR PDB: 1H7I: 16-JUN-97.
DR PDB: 1H7J: 16-JUN-97.
DR PDB: 1H7K: 16-JUN-97.
DR PDB: 1H7L: 16-JUN-97.
DR PDB: 1H7M: 16-JUN-97.
DR PDB: 1H7N: 16-JUN-97.
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Molecular output not generated.

Release 3.1a John F. Collins, Blocomputing Research Unit.
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Mparch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 09:56:12 1998; Maspar time 3.80 Seconds
110.885 Million cell updates/sec

Molecular output not generated.

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68
Sequence: 1 SVSEIQLMHN 10

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: spiremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.590; Variance 21.849; scale 1.034

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Query Length	DB ID	Description	Pred. No.
1	64.1	105	10	063473	PARATHYROID HORMONE (F	5.68e-05
2	48	70.6	248	008320	ACETYLGLUTAMATE KINASE	1.66e+00
3	48	70.6	448	055883	HYPOTHETICAL 49.8 KD P	1.66e+00
4	48	70.6	1015	014521	GIANT LARYAE HOMOLOGUE	2.96e+00
5	47	69.1	2668	020456	F46C3.3.	2.96e+00
6	46	67.6	445	2	UNDULIN 2 (MATRIX GLYC	5.23e+00
7	46	67.6	843	2	UNDULIN 1 (MATRIX GLYC	5.23e+00
8	46	67.6	1034	10	LETHAL GIANT LARYAE HO	5.23e+00
9	46	67.6	1371	9	SENSORY TRANSDUCTION H	9.15e+00
10	45	66.2	276	3	SIMILAR TO TYROSINE KI	9.15e+00
11	45	66.2	405	9	FROM BASES 2347342 TO	9.15e+00
12	45	66.2	821	9	GLYCOGEN PHOSPHORYLASE	9.15e+00
13	45	66.2	1405	10	STERIOD RECEPTOR COACT	9.15e+00
14	45	66.2	1405	10	STERIOD RECEPTOR COACT	9.15e+00
15	45	66.2	1441	2	NUCLEAR RECEPTOR CO-AC	9.15e+00
16	45	66.2	1447	10	HYPOTHETICAL 11.5 KD P	1.59e+01
17	44	64.7	99	9	FBP PROTEIN.	1.59e+01
18	44	64.7	247	8	AGAMOUS PROTEIN.	1.59e+01
19	44	64.7	267	9	DIIHDROPTERATE SYNTHA	1.59e+01
20	44	64.7	267	9	DIIHDROPTERATE SYNTHA	1.59e+01

21	44	64.7	402	9	055818	HYPOTHETICAL 45.8 KD P	1.59e+01
22	44	64.7	407	3	019956	SIMILARITY TO S. CERVI	1.59e+01
23	44	64.7	448	9	031012	OFFSIX5 PROTEIN.	1.59e+01
24	44	64.7	451	8	041789	CALCIUM-DEPENDENT PROT	1.59e+01
25	44	64.7	483	8	039014	CALCIUM-DEPENDENT PROT	1.59e+01
26	44	64.7	487	8	043676	CALCIUM-DEPENDENT PROT	1.59e+01
27	44	64.7	490	8	042396	CALCIUM-DEPENDENT PROT	1.59e+01
28	44	64.7	490	8	024430	CALMODULIN-LIKE DOMAIN	1.59e+01
29	44	64.7	492	8	004417	CALCIUM-DEPENDENT PROT	1.59e+01
30	44	64.7	495	8	039016	CALCIUM-DEPENDENT PROT	1.59e+01
31	44	64.7	501	8	038869	CALMODULIN-DOMAIN PROT	1.59e+01
32	44	64.7	544	8	038872	CALMODULIN-DOMAIN PROT	1.59e+01
33	44	64.7	554	8	004123	CALCIUM-DEPENDENT PROT	1.59e+01
34	44	64.7	556	8	038871	CALMODULIN-DOMAIN PROT	1.59e+01
35	44	64.7	573	8	038871	CALCIUM-DEPENDENT CALM	1.59e+01
36	44	64.7	646	8	038870	CALMODULIN-DOMAIN PROT	1.59e+01
37	43	63.2	167	9	096578	YDAE PROTEIN.	2.72e+01
38	43	63.2	199	9	018251	Y7G11C.25.	2.72e+01
39	43	63.2	226	9	094331	RGA.	2.72e+01
40	43	63.2	737	3	017679	CA9F5.2.	2.72e+01
41	43	63.2	818	11	088272	NON-STRUCTURAL PROTEIN	2.72e+01
42	43	63.2	911	11	083905	TERMINAL PROTEIN.	2.72e+01
43	43	63.2	1057	2	015334	TUMOUR SUPPRESSOR PROT	2.72e+01
44	43	63.2	2500	3	020937	SIMILAR TO S. CREVISTI	2.72e+01
45	43	63.2	3436	11	089201	POLYPROTEIN.	2.72e+01

ALIGNMENTS

RESULT	ID	063473	PRELIMINARY	PRT	105 AA.
AC	063473	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE (FRAGMENT).				
GN	PTH.				
OS	RATVUS NORVEGICUS (RAT).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;				
OC	EUTHIRIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TTSSE-THYROID, AND PARATHYROID.				
RA	SCHMELZER H.J., GROSS G., MAYER H.;				
RL	ADV. GENE TECHNOL. 21:228-229(1984).				
DR	EMBL; M54875; G601933; -.				
FT	NON TER				
SQ	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;				
Query Match					
Best Local Similarity 80.0%; Pred. No. 5.68e-05;					
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;					
Db	22 AISIQLMHN 31				
QY	1 SVSEIQLMHN 10				
RESULT	2	PRELIMINARY	PRT	248 AA.	
ID	008320				
AC	008320	01-JUL-1997 (TREMBLREL. 04, CREATED)			
DT	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				
DE	ACETYLGLUTAMATE KINASE (EC 2.7.2.8).				
GN	ARGB.				
OS	LACTOBACILLUS PLANTARUM.				
OC	PROKARYOTA; FIRMICUTES; REGULAR ASPOROGENOUS ROD; LACTOBACILLACEAE.				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RA	STRAIN-COM 1904.				
RL	BRINGEL F., FREY L., BOYIN S., HUBERT J.C.;				
RL	J. BACTERIOL. 179:0-0(1997).				

US-08-817-547A-1.rspt

Thu Jul 30 13:37:52 1998

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CCM 1904;
RA BRINGEL F.; TO EMBL/GENBANK/DBJ DATA BANKS.
RL SUBMITTED (AUG-1996)
CC -1- CATALYTIC ACTIVITY: ATP + N-ACETYL-L-GLUTAMATE =
   ADP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.
DR EMBL: X99978; E284231; -.
KW TRANSFERASE
SQ SEQUENCE 248 AA; 26580 MM; 3E945D79 CRC32;

Query Match 70.6%; Score 48; DB 9; Length 248;
Best Local Similarity 44.4%; Pred. No. 1.66e+00; Indels 0;
Matches 4; Conservative 5; Mismatches 0; Gaps 0;

Db 125 AVNOYOLMQ 133
OY 1 SYSEIOLMH 9

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Search completed: Thu Jul 30 09:56:47 1998
 Job time : 35 secs.

M O S E R
(TW)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 09:59:58 1998; MasPar time 2.62 Seconds
52.740 Million cell updates/sec
Molecular output not generated.

Title: >US-08-817-547A-2
Description: (1-9) from US08817547A.pep
Perfect Score: 63
Sequence: 1 SVSEIQLMH 9

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.754; Variance 60.392; scale 0.261
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	63	100.0	34	22	W17954	Human parathyroid hor	9.63e+00
2	63	100.0	34	22	W17955	Human parathyroid hor	9.63e+00
3	63	100.0	34	23	W08127	Human PTH derivative,	9.63e+00
4	63	100.0	34	23	W08102	Parathyroid hormone g	9.63e+00
5	63	100.0	34	7	R34366	Human parathyroid hor	9.63e+00
6	63	100.0	34	7	R34362	Human parathyroid hor	9.63e+00
7	63	100.0	34	20	W14310	Cyclic parathyroid ho	9.63e+00
8	63	100.0	34	20	W14309	Cyclic parathyroid ho	9.63e+00
9	63	100.0	34	22	W17969	Human parathyroid hor	9.63e+00
10	63	100.0	34	22	W17951	Human parathyroid hor	9.63e+00
11	63	100.0	34	22	W17967	Human PTH analogue (C	9.63e+00
12	63	100.0	34	22	W17968	Human parathyroid hor	9.63e+00
13	63	100.0	34	22	W17947	Human parathyroid hor	9.63e+00
14	63	100.0	34	22	W17944	Human parathyroid hor	9.63e+00
15	63	100.0	34	22	W17952	Human parathyroid hor	9.63e+00
16	63	100.0	34	23	W08114	Human PTH derivative,	9.63e+00
17	63	100.0	34	22	W19994	Cyclised human parath	9.63e+00
18	63	100.0	34	7	R34365	Human parathyroid hor	9.63e+00
19	63	100.0	34	7	R34364	Human parathyroid hor	9.63e+00

RESULT	ID	Score	Query Match	length	DB	ID	Description	Pred. No.
20	63	100.0	34	7	R34354	Human parathyroid hor	9.63e+00	
21	63	100.0	34	7	R34353	Human parathyroid hor	9.63e+00	
22	63	100.0	36	9	R58229	[Ala30]-hPTH(1-36)-NH	9.63e+00	
23	63	100.0	36	9	R58298	[NMeVal35]-hPTH(1-36)	9.63e+00	
24	63	100.0	36	9	R58284	[D-Trp23]-hPTH(1-36)-	9.63e+00	
25	63	100.0	36	9	R58284	[Lys(Iso-propyl)13]-hP	9.63e+00	
26	63	100.0	36	9	R58281	[D-Val21]-hPTH(1-36)-	9.63e+00	
27	63	100.0	36	9	R58234	[Ala32]-hPTH(1-36)-NH	9.63e+00	
28	63	100.0	36	9	R58233	[D-His32]-hPTH(1-36)-	9.63e+00	
29	63	100.0	36	8	R39450	Ser-Val-(hPTH 3-35)-P	9.63e+00	
30	63	100.0	36	9	R58274	[Ala15]-hPTH(1-36)-NH	9.63e+00	
31	63	100.0	37	9	R58244	[Ala20]-hPTH(1-36)-NH	9.63e+00	
32	63	100.0	37	9	R24776	hPTH(1-37)-amide/ethy	9.63e+00	
33	63	100.0	38	9	R58283	[Trp(Pmc)23]-hPTH(1-3	9.63e+00	
34	63	100.0	38	9	R58094	[Trp13]-hPTH(1-38)-OH	9.63e+00	
35	63	100.0	38	9	R58093	[Asn13]-hPTH(1-38)-OH	9.63e+00	
36	63	100.0	38	9	R58166	[Lys33]-hPTH(1-38)-OH	9.63e+00	
37	63	100.0	38	9	R58282	[Trp(SQ2Pmc)23]-hPTH	9.63e+00	
38	63	100.0	38	9	R58061	[Ile15]-hPTH(1-38)-OH	9.63e+00	
39	63	100.0	44	26	P30015	Human parathyroid hor	9.63e+00	
40	63	100.0	47	25	W21946	Fusion protein compri	9.63e+00	
41	63	100.0	84	27	W25687	Human parathyroid hor	9.63e+00	
42	63	100.0	84	25	W29420	Human parathyroid hor	9.63e+00	
43	63	100.0	84	4	R23790	Parathyroid hormone g	9.63e+00	
44	63	100.0	84	5	R23571	Human PTH encoded by	9.63e+00	
45	63	100.0	229	9	R47971	Sequence of a full-le	9.63e+00	

ALIGNMENTS

RESULT 1
ID W17954 standard; peptide; 34 AA.
AC W17954;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Alb19]hPTH(1-34)NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW Bone fracture.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 19
FT modified_site 19 label= Alb
FT modified_site 34
FT modified_site 34 /note= "In amide form"
FN WO9702834-A1.
PD 30-JAN-1997.
PF 03-JUL-1996; U11292.
PR 13-JUL-1995; US-001105.
PR 06-SEP-1995; US-003305.
PR 29-MAR-1996; US-626186.
PA (BIOM-) BIOMEASURE INC.
PI Dong ZX;
DR WPI: 97-118819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which
stimulate bone growth and are used for treatment of osteoporosis and
bone fracture
PS Claim 11: Page -: 33pp; English.
CC The present sequence is a specific example of a human parathyroid
hormone (hPTH) analogue from fragment 1-34 in which at least one
of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
is alpha-aminoisobutyric acid (Aib). In this example the Glu residue
at position 19 of the wild-type has been substituted by Aib. The hPTH
analogues stimulate bone growth and so are useful in human or veterinary
medicine for treatment of osteoporosis and bone fracture, optionally in
conjunction with anti-resorptive therapy (bisphosphonates and
calcitonin).
CC N.B. The present sequence does not appear in the specification. It
corresponds to the known hPTH 1-34 fragment with the modifications
as stated in the claim.
SQ Sequence 34 AA;
Query Match 100.0%; Score 63; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.63e+00.

Thu Jul 30 13:38:01 1998

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 svseiqjmh 9
 |||||
 QY 1 SVSEIQJMH 9

RESULT 2
 ID W17955 standard; peptide; 34 AA.

AC W17955:
 DT 29-JUL-1997 (first entry)
 DE Human parathyroid hormone analogue [Alb34]hPTH(1-34)NH2;
 KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 OS bone fracture.
 OS Homo sapiens.
 OS Synthetic.
 FT modified_site 34 Location/Qualifiers
 Key /label= Alb
 /note= "in amide form"

MO9702834-A1.
 PD 30-JAN-1997. U11292.
 PF 03-JUL-1996; US-001105.
 PR 13-JUL-1995; US-003305.
 PR 06-SEP-1995; US-626186.
 PR 29-MAR-1996; US-626186.
 PA (BIOM-) BIOMEASURE INC.
 PI Dong 2X;
 DR WPI; 97-118819/11.
 PR New variants of human parathyroid hormone 1-34 peptide - which
 stimulate bone growth and are used for treatment of osteoporosis and
 bone fracture.
 PS Claim 11: Page -: 33pp: English.
 CC The present sequence is a specific example of a human parathyroid
 hormone (hPTH) analogue from fragment 1-34 in which at least one
 of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
 is alpha-aminoisobutyric acid (Aib). In this example the Phe residue
 at position 34 of the wild-type has been substituted by Aib. The hPTH
 analogues stimulate bone growth and so are useful in human or veterinary
 medicine for treatment of osteoporosis and bone fracture, optionally in
 conjunction with anti-resorptive therapy (bisphosphonates and
 calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 corresponds to the known hPTH 1-34 fragment with the modifications
 as stated in the claim.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 63; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 9.63e+00; Mismatches 0; Indels 0;
 Matches 9; Conservative

Db 1 svseiqjmh 9
 |||||
 QY 1 SVSEIQJMH 9

Search completed: Thu Jul 30 10:00:14 1998
 Job time : 16 secs.

NWSETH (TM)

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Msrch_p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 09:59:20 1998; Maspar time 3.14 Seconds
104.825 Million cell updates/sec
Molar output not generated.

Title: >US-08-817-547A-2
Description: (1-9) from US08817547A.pep
Perfect Score: 63
Sequence: 1 SVSEIQLMH 9

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:m1r3d

Statistics: Mean 21.980; Variance 26.868; scale 0.818

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	63	100.0	34	5	1LWA parathyroid hormone (2.58e-03	
2	63	100.0	37	5	1HPH parathyroid hormone f (2.58e-03	
3	63	100.0	115	1	1PTHU parathyroid hormone f (2.58e-03	
4	63	100.0	115	1	1PRPG parathyroid hormone p (2.58e-03	
5	61	96.8	115	2	A05091 parathyroid hormone p (7.78e-03	
6	59	93.7	106	5	1LWB parathyroid hormone (2.31e-02	
7	59	93.7	105	2	151851 parathyroid hormone (3.94e-02	
8	58	92.1	119	2	A34937 parathyroid hormone p (3.94e-02	
9	56	88.9	115	2	JC4202 parathyroid hormone p (1.14e-01	
10	54	85.7	37	5	1LWC parathyroid hormone (3.21e-01	
11	54	85.7	115	1	1PTBO parathyroid hormone p (3.21e-01	
12	52	82.5	34	5	1HTH cyclic parathyroid ho (8.88e-01	
13	52	82.5	35	5	1LWD parathyroid hormone (8.88e-01	
14	48	76.2	34	5	1LWE parathyroid hormone (6.33e+00	
15	48	76.2	34	5	1LWF parathyroid hormone (6.33e+00	
16	48	76.2	34	5	1LWG parathyroid hormone (6.33e+00	
17	48	76.2	1015	2	S55474 Human giant larvae ho (6.33e+00	
18	47	74.6	383	2	B42377 acetylornithine deace (1.02e+01	
19	47	74.6	448	2	S76701 hypothetical protein (1.02e+01	
20	46	73.0	445	2	B40970 undulin 2 - human (fr (1.62e+01	
21	46	73.0	843	2	A40970 undulin 1 - human (fr (1.62e+01	
22	46	73.0	1034	2	S36758 mg11 protein - mouse (1.62e+01	
23	45	71.4	132	2	S14236 Ig gamma-1 chain C re (2.57e+01	

24	45	71.4	324	1	G1MS	Ig gamma-1 chain C re	2.57e+01
25 <td>45<td>71.4<td>393<td>1<td>G1MSM<td>Ig gamma-1 chain C re<th>2.57e+01</th></td></td></td></td></td></td>	45 <td>71.4<td>393<td>1<td>G1MSM<td>Ig gamma-1 chain C re<th>2.57e+01</th></td></td></td></td></td>	71.4 <td>393<td>1<td>G1MSM<td>Ig gamma-1 chain C re<th>2.57e+01</th></td></td></td></td>	393 <td>1<td>G1MSM<td>Ig gamma-1 chain C re<th>2.57e+01</th></td></td></td>	1 <td>G1MSM<td>Ig gamma-1 chain C re<th>2.57e+01</th></td></td>	G1MSM <td>Ig gamma-1 chain C re<th>2.57e+01</th></td>	Ig gamma-1 chain C re <th>2.57e+01</th>	2.57e+01
26 <td>45<td>71.4<td>444<td>2<td>PC4436<td>monoclonal antibody 1<th>2.57e+01</th></td></td></td></td></td></td>	45 <td>71.4<td>444<td>2<td>PC4436<td>monoclonal antibody 1<th>2.57e+01</th></td></td></td></td></td>	71.4 <td>444<td>2<td>PC4436<td>monoclonal antibody 1<th>2.57e+01</th></td></td></td></td>	444 <td>2<td>PC4436<td>monoclonal antibody 1<th>2.57e+01</th></td></td></td>	2 <td>PC4436<td>monoclonal antibody 1<th>2.57e+01</th></td></td>	PC4436 <td>monoclonal antibody 1<th>2.57e+01</th></td>	monoclonal antibody 1 <th>2.57e+01</th>	2.57e+01
27 <td>45<td>71.4<td>1371<td>2<td>S77521<td>sensory transduction<th>2.57e+01</th></td></td></td></td></td></td>	45 <td>71.4<td>1371<td>2<td>S77521<td>sensory transduction<th>2.57e+01</th></td></td></td></td></td>	71.4 <td>1371<td>2<td>S77521<td>sensory transduction<th>2.57e+01</th></td></td></td></td>	1371 <td>2<td>S77521<td>sensory transduction<th>2.57e+01</th></td></td></td>	2 <td>S77521<td>sensory transduction<th>2.57e+01</th></td></td>	S77521 <td>sensory transduction<th>2.57e+01</th></td>	sensory transduction <th>2.57e+01</th>	2.57e+01
28 <td>44<td>69.8<td>99<td>2<td>C64489<td>hypothetical protein<th>4.05e+01</th></td></td></td></td></td></td>	44 <td>69.8<td>99<td>2<td>C64489<td>hypothetical protein<th>4.05e+01</th></td></td></td></td></td>	69.8 <td>99<td>2<td>C64489<td>hypothetical protein<th>4.05e+01</th></td></td></td></td>	99 <td>2<td>C64489<td>hypothetical protein<th>4.05e+01</th></td></td></td>	2 <td>C64489<td>hypothetical protein<th>4.05e+01</th></td></td>	C64489 <td>hypothetical protein<th>4.05e+01</th></td>	hypothetical protein <th>4.05e+01</th>	4.05e+01
29 <td>44<td>69.8<td>553<td>1<td>TLBP57<td>tail fiber protein<th>4.05e+01</th></td></td></td></td></td></td>	44 <td>69.8<td>553<td>1<td>TLBP57<td>tail fiber protein<th>4.05e+01</th></td></td></td></td></td>	69.8 <td>553<td>1<td>TLBP57<td>tail fiber protein<th>4.05e+01</th></td></td></td></td>	553 <td>1<td>TLBP57<td>tail fiber protein<th>4.05e+01</th></td></td></td>	1 <td>TLBP57<td>tail fiber protein<th>4.05e+01</th></td></td>	TLBP57 <td>tail fiber protein<th>4.05e+01</th></td>	tail fiber protein <th>4.05e+01</th>	4.05e+01
30 <td>44<td>69.8<td>557<td>1<td>TLBP73<td>tail fiber protein -<th>4.05e+01</th></td></td></td></td></td></td>	44 <td>69.8<td>557<td>1<td>TLBP73<td>tail fiber protein -<th>4.05e+01</th></td></td></td></td></td>	69.8 <td>557<td>1<td>TLBP73<td>tail fiber protein -<th>4.05e+01</th></td></td></td></td>	557 <td>1<td>TLBP73<td>tail fiber protein -<th>4.05e+01</th></td></td></td>	1 <td>TLBP73<td>tail fiber protein -<th>4.05e+01</th></td></td>	TLBP73 <td>tail fiber protein -<th>4.05e+01</th></td>	tail fiber protein - <th>4.05e+01</th>	4.05e+01
31 <td>43<td>68.3<td>103<td>2<td>D64034<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>103<td>2<td>D64034<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>103<td>2<td>D64034<td>hypothetical protein<th>6.32e+01</th></td></td></td></td>	103 <td>2<td>D64034<td>hypothetical protein<th>6.32e+01</th></td></td></td>	2 <td>D64034<td>hypothetical protein<th>6.32e+01</th></td></td>	D64034 <td>hypothetical protein<th>6.32e+01</th></td>	hypothetical protein <th>6.32e+01</th>	6.32e+01
32 <td>43<td>68.3<td>167<td>2<td>E69768<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>167<td>2<td>E69768<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>167<td>2<td>E69768<td>hypothetical protein<th>6.32e+01</th></td></td></td></td>	167 <td>2<td>E69768<td>hypothetical protein<th>6.32e+01</th></td></td></td>	2 <td>E69768<td>hypothetical protein<th>6.32e+01</th></td></td>	E69768 <td>hypothetical protein<th>6.32e+01</th></td>	hypothetical protein <th>6.32e+01</th>	6.32e+01
33 <td>43<td>68.3<td>225<td>2<td>S77105<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>225<td>2<td>S77105<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>225<td>2<td>S77105<td>hypothetical protein<th>6.32e+01</th></td></td></td></td>	225 <td>2<td>S77105<td>hypothetical protein<th>6.32e+01</th></td></td></td>	2 <td>S77105<td>hypothetical protein<th>6.32e+01</th></td></td>	S77105 <td>hypothetical protein<th>6.32e+01</th></td>	hypothetical protein <th>6.32e+01</th>	6.32e+01
34 <td>43<td>68.3<td>247<td>2<td>S60307<td>fbp6 protein - garden<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>247<td>2<td>S60307<td>fbp6 protein - garden<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>247<td>2<td>S60307<td>fbp6 protein - garden<th>6.32e+01</th></td></td></td></td>	247 <td>2<td>S60307<td>fbp6 protein - garden<th>6.32e+01</th></td></td></td>	2 <td>S60307<td>fbp6 protein - garden<th>6.32e+01</th></td></td>	S60307 <td>fbp6 protein - garden<th>6.32e+01</th></td>	fbp6 protein - garden <th>6.32e+01</th>	6.32e+01
35 <td>43<td>68.3<td>402<td>2<td>S76529<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>402<td>2<td>S76529<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>402<td>2<td>S76529<td>hypothetical protein<th>6.32e+01</th></td></td></td></td>	402 <td>2<td>S76529<td>hypothetical protein<th>6.32e+01</th></td></td></td>	2 <td>S76529<td>hypothetical protein<th>6.32e+01</th></td></td>	S76529 <td>hypothetical protein<th>6.32e+01</th></td>	hypothetical protein <th>6.32e+01</th>	6.32e+01
36 <td>43<td>68.3<td>651<td>2<td>S47750<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>651<td>2<td>S47750<td>hypothetical protein<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>651<td>2<td>S47750<td>hypothetical protein<th>6.32e+01</th></td></td></td></td>	651 <td>2<td>S47750<td>hypothetical protein<th>6.32e+01</th></td></td></td>	2 <td>S47750<td>hypothetical protein<th>6.32e+01</th></td></td>	S47750 <td>hypothetical protein<th>6.32e+01</th></td>	hypothetical protein <th>6.32e+01</th>	6.32e+01
37 <td>43<td>68.3<td>1057<td>2<td>I38171<td>hug1 protein - human<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>1057<td>2<td>I38171<td>hug1 protein - human<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>1057<td>2<td>I38171<td>hug1 protein - human<th>6.32e+01</th></td></td></td></td>	1057 <td>2<td>I38171<td>hug1 protein - human<th>6.32e+01</th></td></td></td>	2 <td>I38171<td>hug1 protein - human<th>6.32e+01</th></td></td>	I38171 <td>hug1 protein - human<th>6.32e+01</th></td>	hug1 protein - human <th>6.32e+01</th>	6.32e+01
38 <td>43<td>68.3<td>1134<td>1<td>JN0711<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>1134<td>1<td>JN0711<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>1134<td>1<td>JN0711<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td></td>	1134 <td>1<td>JN0711<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td>	1 <td>JN0711<td>protein-tyrosine kina<th>6.32e+01</th></td></td>	JN0711 <td>protein-tyrosine kina<th>6.32e+01</th></td>	protein-tyrosine kina <th>6.32e+01</th>	6.32e+01
39 <td>43<td>68.3<td>1136<td>1<td>S57845<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>1136<td>1<td>S57845<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>1136<td>1<td>S57845<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td></td>	1136 <td>1<td>S57845<td>protein-tyrosine kina<th>6.32e+01</th></td></td></td>	1 <td>S57845<td>protein-tyrosine kina<th>6.32e+01</th></td></td>	S57845 <td>protein-tyrosine kina<th>6.32e+01</th></td>	protein-tyrosine kina <th>6.32e+01</th>	6.32e+01
40 <td>43<td>68.3<td>2163<td>2<td>S50675<td>pre-mRNA splicing hel<th>6.32e+01</th></td></td></td></td></td></td>	43 <td>68.3<td>2163<td>2<td>S50675<td>pre-mRNA splicing hel<th>6.32e+01</th></td></td></td></td></td>	68.3 <td>2163<td>2<td>S50675<td>pre-mRNA splicing hel<th>6.32e+01</th></td></td></td></td>	2163 <td>2<td>S50675<td>pre-mRNA splicing hel<th>6.32e+01</th></td></td></td>	2 <td>S50675<td>pre-mRNA splicing hel<th>6.32e+01</th></td></td>	S50675 <td>pre-mRNA splicing hel<th>6.32e+01</th></td>	pre-mRNA splicing hel <th>6.32e+01</th>	6.32e+01
41 <td>42<td>66.7<td>116<td>2<td>S22553<td>Ig heavy chain V regi<th>9.79e+01</th></td></td></td></td></td></td>	42 <td>66.7<td>116<td>2<td>S22553<td>Ig heavy chain V regi<th>9.79e+01</th></td></td></td></td></td>	66.7 <td>116<td>2<td>S22553<td>Ig heavy chain V regi<th>9.79e+01</th></td></td></td></td>	116 <td>2<td>S22553<td>Ig heavy chain V regi<th>9.79e+01</th></td></td></td>	2 <td>S22553<td>Ig heavy chain V regi<th>9.79e+01</th></td></td>	S22553 <td>Ig heavy chain V regi<th>9.79e+01</th></td>	Ig heavy chain V regi <th>9.79e+01</th>	9.79e+01
42 <td>42<td>66.7<td>176<td>2<td>S27182<td>retinol-binding prote<th>9.79e+01</th></td></td></td></td></td></td>	42 <td>66.7<td>176<td>2<td>S27182<td>retinol-binding prote<th>9.79e+01</th></td></td></td></td></td>	66.7 <td>176<td>2<td>S27182<td>retinol-binding prote<th>9.79e+01</th></td></td></td></td>	176 <td>2<td>S27182<td>retinol-binding prote<th>9.79e+01</th></td></td></td>	2 <td>S27182<td>retinol-binding prote<th>9.79e+01</th></td></td>	S27182 <td>retinol-binding prote<th>9.79e+01</th></td>	retinol-binding prote <th>9.79e+01</th>	9.79e+01
43 <td>42<td>66.7<td>176<td>2<td>S10202<td>parathyroid hormone-r<th>9.79e+01</th></td></td></td></td></td></td>	42 <td>66.7<td>176<td>2<td>S10202<td>parathyroid hormone-r<th>9.79e+01</th></td></td></td></td></td>	66.7 <td>176<td>2<td>S10202<td>parathyroid hormone-r<th>9.79e+01</th></td></td></td></td>	176 <td>2<td>S10202<td>parathyroid hormone-r<th>9.79e+01</th></td></td></td>	2 <td>S10202<td>parathyroid hormone-r<th>9.79e+01</th></td></td>	S10202 <td>parathyroid hormone-r<th>9.79e+01</th></td>	parathyroid hormone-r <th>9.79e+01</th>	9.79e+01
44 <td>42<td>66.7<td>579<td>2<td>S54872<td>penicillin-binding pr<th>9.79e+01</th></td></td></td></td></td></td>	42 <td>66.7<td>579<td>2<td>S54872<td>penicillin-binding pr<th>9.79e+01</th></td></td></td></td></td>	66.7 <td>579<td>2<td>S54872<td>penicillin-binding pr<th>9.79e+01</th></td></td></td></td>	579 <td>2<td>S54872<td>penicillin-binding pr<th>9.79e+01</th></td></td></td>	2 <td>S54872<td>penicillin-binding pr<th>9.79e+01</th></td></td>	S54872 <td>penicillin-binding pr<th>9.79e+01</th></td>	penicillin-binding pr <th>9.79e+01</th>	9.79e+01
45 <td>42<td>66.7<td>619<td>2<td>I59558<td>dopamine transporter<th>9.79e+01</th></td></td></td></td></td></td>	42 <td>66.7<td>619<td>2<td>I59558<td>dopamine transporter<th>9.79e+01</th></td></td></td></td></td>	66.7 <td>619<td>2<td>I59558<td>dopamine transporter<th>9.79e+01</th></td></td></td></td>	619 <td>2<td>I59558<td>dopamine transporter<th>9.79e+01</th></td></td></td>	2 <td>I59558<td>dopamine transporter<th>9.79e+01</th></td></td>	I59558 <td>dopamine transporter<th>9.79e+01</th></td>	dopamine transporter <th>9.79e+01</th>	9.79e+01

ALIGNMENTS

RESULT	1	12WA	#type complete
ENTRY	parathyroid hormone (residues 1-34) - human		
TITLE	HPTH(1-34)		
ALTERNATE_NAMES	structure of human parathyroid hormone fragment 1-34, NMR 10		
PDB_TITLE	structures		
ORGANISM	#formal_name Homo sapiens #common_name man		
REFERENCE	A67856		
#authors	Roesch, P.; Marx, U.C.		
#submission	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WA		
REFERENCE	TN001717		
#authors	Marx, U.C.		
#book	In Struktur und Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996		
COMMENT	Resolution: not applicable		
COMMENT	Determination: NMR		
FEATURE	hormone		
FEATURE	6-9		
SUMMARY	19-30		
	#region helix (right hand alpha)\		
	#region helix (right hand alpha)		
	#length 34 #molecular-weight 4118 #checksum 5629		
Query Match	100.0%; Score 63; DB 5; Length 34;		
Best local Similarity	100.0%; Pred. No. 2.58e-03;		
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	1 SVSEIQLMH 9		
QY	1 SVSEIQLMH 9		
RESULT	2		
ENTRY	1HPH	#type complete	
TITLE	parathyroid hormone fragment 1 37 (hpth(1-37)) (NMR, 10		
ORGANISM	structures) - synthetic		
REFERENCE	#formal_name synthetic		
A65802			
#authors	Marx, U.C.; Roesch, P.		
#submission	submitted to the Brookhaven Protein Data Bank, February 1995		
#cross-references	PDB:1HPH		
COMMENT	Resolution: not applicable		
COMMENT	Determination: NMR		
COMMENT	R-value: no refinement		
KEYWORDS	hormone		
FEATURE	6-9		
	#region helix (right hand alpha)\		

US-08-817-547A-2.rpt

Thu Jul 30 13:38:02 1998

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17-28      #region helix (right hand alpha)
SUMMARY    #length 37 #molecular-weight 4401 #checksum 3791
Query Match      100.0%; Score 63; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.58e-03; Indels 0; Gaps 0;
Matches          9; Conservative 0; Mismatches 0;
Db      1 SVSEIQLMH 9
Oy      1 SVSEIQLMH 9

Search completed: Thu Jul 30 09:59:39 1998
Job time : 19 secs.

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MUSE (TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jul 30 09:58:20 1998; Maspar time 2.06 Seconds
Molecular output not generated. 109.762 Million cell updates/sec

Title: >US-08-817-547A-2
Description: (1-9) from US08817547A.pep
Perfect Score: 63
Sequence: 1 SVSEIOLMH 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.879; Variance 22.094; scale 1.0316

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	63	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	7.43e-05
2	63	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	7.43e-05
3	61	96.8	115	1	PTHY_RAT PARATHYROID HORMONE PR	2.88e-04
4	58	92.1	119	1	PTHY_CHICK PARATHYROID HORMONE PR	2.11e-03
5	56	88.9	115	1	PTHY_CANFA PARATHYROID HORMONE PR	7.68e-03
6	54	85.7	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	2.73e-02
7	50	79.4	369	1	PROB_CORGL GLUTAMATE 5-KINASE (EC	3.16e-01
8	47	74.6	383	1	ARCE_ECOLI ACETYLCHOLINE DEACET	1.81e+00
9	47	74.6	435	1	Y413_ARATH HYPOTHETICAL 48.8 KD P	1.81e+00
10	45	71.4	324	1	GCL_MOUSE IG GAMMA-1 CHAIN C REG	5.55e+00
11	45	71.4	393	1	GC1A_MOUSE IG GAMMA-1 CHAIN C REG	5.55e+00
12	44	69.8	151	1	LE14_GOSHI LATE EMBRYOGENESIS ABU	9.57e+00
13	44	69.8	553	1	VTFP_BPT7 TAIL FIBER PROTEIN.	9.57e+00
14	44	69.8	557	1	VTFP_BPT7 TAIL FIBER PROTEIN.	9.57e+00
15	43	68.3	103	1	YF17_HAEIN HYPOTHETICAL 73.1 KD P	1.63e+01
16	43	68.3	651	1	YHJK_ECOLI HYPOTHETICAL 73.1 KD P	1.63e+01
17	43	68.3	1069	1	ENTR_MOUSE ENTEROPEPTIDASE (EC 3.	1.63e+01
18	43	68.3	1136	1	TIEL_MOUSE TYROSINE-PROTEIN KINAS	1.63e+01
19	43	68.3	1134	1	TIEL_MOUSE TYROSINE-PROTEIN KINAS	1.63e+01
20	43	68.3	2163	1	BRR2_YEAST PRE-RNA SPLICING HELI	2.76e+01
21	42	66.7	175	1	PTHY_MOUSE PARATHYROID HORMONE-RE	2.76e+01
22	42	66.7	176	1	RET1_ONCMY PLASMA RETINOL-BINDING	2.76e+01
23	42	66.7	176	1	RET2_ONCMY PLASMA RETINOL-BINDING	2.76e+01

RESULT	ID	PTHY_HUMAN	STANDARD	PRT	115 AA.	ALIGNMENTS
AC	P01270:					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUHETERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.;					
RL	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RA	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RA	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;					
RL	O'RiORDAN J.L.H., AUBACH G.D., POTTS J.T. JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RiORDAN J.L.H.;					
RL	POTTS J.T. JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;					
RA	O'RiORDAN J.L.H., POTTS J.T. JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.;					
RL	PARSONS J.A., EDS., PP. 9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGER G.W., VAN RIENSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDERLETTA R.H., HARTMANN A., JOEHL A., KAMBER B., WAIER R.,
 RA RINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345518.
 RA BARDEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MARK U.C., AUSSERMAN S., BAYER P., ADERMAN K., EICHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 CC EMBL: J00301; G190704; -;
 DR EMBL: V00597; G37144; -;
 DR EMBL: A29146; E186700; -;
 DR PIR: A01536; PTHU.
 DR PIR: A19339; A19339.
 DR PDB: 1HPH: 10-JUL-95.
 DR PDB: 1HTH: 15-OCT-97.
 DR PDB: 1ZMA: 12-MAR-97.
 DR PDB: 1ZMB: 12-MAR-97.
 DR PDB: 1ZMC: 12-MAR-97.
 DR PDB: 1ZMD: 12-MAR-97.
 DR PDB: 1ZME: 12-MAR-97.
 DR PDB: 1ZMF: 16-JUN-97.
 DR PDB: 1ZMG: 16-JUN-97.
 DR MTM: 146200; -;
 DR MTM: 168450; -;
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR KW HORMONE; SIGNAL; DISPERSE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA: 12861 MW: 243887C7 CRC32;
 SQ
 Query Match 100.0%; Score 63; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 7.43e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 32 SVSEIQLMH 40
 1111111111
 QY 1 SVSEIQLMH 9
 RESULT 2
 ID PTHY_PIG STANDARD; PRT: 115 AA.
 AC P01269;
 DC 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS SUS SCROFA (Pig).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87316938.
 RA SCHWEIZER H.-J., GROSS G., WIEDER G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN [2]
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN [3]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 74253317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 RA POTTS J.T. JR.;
 RL BIOCHEMISTRY 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL: X05722; G1839; -;
 DR PIR: A01535; PTHG.
 DR PIR: B26806; B26806.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR KW HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT SEQUENCE 115 AA: 12852 MW: 98867F47 CRC32;
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 Best Local Similarity 100.0%; Pred. No. 7.43e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 32 SVSEIQLMH 40
 1111111111
 QY 1 SVSEIQLMH 9
 Search completed: Thu Jul 30 09:58:27 1998
 Job time : 7 secs.

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MSrch_Pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 09:58:46 1998; Maspar time 3.70 Seconds
102.472 Million cell updates/sec

Title: >US-08-817-547A-2
Description: (1-9) from US08817547A.pep
Perfect Score: 63
Sequence: 1 SVSEIQLMH 9

Scoring table: PAM 150
Gap 15

Searched: 140542 segs. 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_prodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.143; Variance 20.804; scale 1.064

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	59	93.7	105	10	063473	PARATHYROID HORMONE (F	6.56e-04
2	48	76.2	248	9	008320	ACETYLGLUTAMATE KINASE	8.60e-01
3	48	76.2	1015	2	014321	GIANT LARVAE HOMOLOGUE	8.60e-01
4	47	74.6	448	9	005883	HYPOTHETICAL 49.8 KD P	1.57e+00
5	46	73.0	445	2	005708	UNIDULIN 2 (MATRIX GLYC	2.85e+00
6	46	73.0	843	2	005707	UNIDULIN 1 (MATRIX GLYC	2.85e+00
7	45	73.0	1034	10	061856	LETHAL GIANT LARVAE HO	5.12e+00
8	45	71.4	276	3	021996	SIMILAR TO TYROSINE KIN	5.12e+00
9	45	71.4	1371	3	P73337	SENSORY TRANSDUCTION H	5.12e+00
10	45	71.4	1405	10	061202	STEROID RECEPTOR COACT	5.12e+00
11	45	71.4	1405	10	P70366	STEROID RECEPTOR COACT	5.12e+00
12	45	71.4	1441	2	000150	STEROID RECEPTOR COACT	5.12e+00
13	45	71.4	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	5.12e+00
14	44	69.8	99	9	058811	HYPOTHETICAL 11.5 KD P	9.10e+00
15	44	69.8	407	3	019956	STIMILARITY TO S. CERVI	9.10e+00
16	44	69.8	448	9	031012	ORF51X5 PROTEIN.	9.10e+00
17	44	69.8	821	9	031210	GLYCOGEN PHOSPHORYLASE	1.60e+01
18	43	68.3	167	9	P96578	YDAE PROTEIN.	1.60e+01
19	43	68.3	199	3	018251	Y57G11C.25	1.60e+01
20	43	68.3	225	9	P73618	DEOXRIBOSE- PHOSPHATE	1.60e+01

21	43	66.3	247	8	008711	FBP6 PROTEIN.	1.60e+01
22	43	66.3	247	8	040900	AGAROUS PROTEIN.	1.60e+01
23	43	66.3	402	9	055818	HYPOTHETICAL 45.8 KD P	1.60e+01
24	43	66.3	910	11	011421	HEXON PROTEIN.	1.60e+01
25	43	66.3	911	11	083905	TERMINAL PROTEIN.	1.60e+01
26	43	66.3	1057	2	015334	TUMOR SUPPRESSOR PROT	1.60e+01
27	43	66.3	3456	11	P89201	POLIPROTEIN.	1.60e+01
28	42	66.7	256	9	026823	CONSERVED PROTEIN.	2.78e+01
29	42	66.7	405	9	P77215	FROM BASES 2347342 TO	2.78e+01
30	42	66.7	418	3	026662	VERY EARLY BLASTULA PR	2.78e+01
31	42	66.7	446	12	P79926	HEPATOCYTE NUCLEAR FAC	2.78e+01
32	42	66.7	451	8	041789	CALCIUM-DEPENDENT PROT	2.78e+01
33	42	66.7	487	8	043676	CALCIUM-DEPENDENT PROT	2.78e+01
34	42	66.7	490	8	042396	CALCIUM-DEPENDENT PROT	2.78e+01
35	42	66.7	490	8	024430	CALMODULIN-LIKE DOMAIN	2.78e+01
36	42	66.7	492	8	004417	CALCIUM DEPENDENT PROT	2.78e+01
37	42	66.7	501	8	038869	CALMODULIN-DOMAIN PROT	2.78e+01
38	42	66.7	544	8	038872	CALMODULIN-DOMAIN PROT	2.78e+01
39	42	66.7	556	8	038871	CALMODULIN-DOMAIN PROT	2.78e+01
40	42	66.7	564	3	020498	F47A4.3.	2.78e+01
41	42	66.7	573	8	P93838	CALCIUM-DEPENDENT CALM	2.78e+01
42	42	66.7	579	9	051504	PENICILLIN-BINDING PRO	2.78e+01
43	42	66.7	646	8	038870	CALMODULIN-DOMAIN PROT	2.78e+01
44	42	66.7	737	3	017679	C49P5.2.	2.78e+01
45	42	66.7	2500	3	020937	SIMILAR TO S. CEREVISI	2.78e+01

ALIGNMENTS

RESULT	ID	Score	Length	DB	ID	Description	Pred. No.
1	063473	93.7%	105	10	063473	PARATHYROID HORMONE (F	6.56e-04
2	008320	77.8%	248	9	008320	ACETYLGLUTAMATE KINASE	8.60e-01
3	014321	74.6%	448	9	005883	HYPOTHETICAL 49.8 KD P	1.57e+00
4	005708	73.0%	445	2	005708	UNIDULIN 2 (MATRIX GLYC	2.85e+00
5	005707	73.0%	843	2	005707	UNIDULIN 1 (MATRIX GLYC	2.85e+00
6	061856	71.4%	1034	10	061856	LETHAL GIANT LARVAE HO	5.12e+00
7	021996	71.4%	276	3	021996	SIMILAR TO TYROSINE KIN	5.12e+00
8	P73337	71.4%	1371	3	P73337	SENSORY TRANSDUCTION H	5.12e+00
9	061202	71.4%	1405	10	061202	STEROID RECEPTOR COACT	5.12e+00
10	P70366	71.4%	1405	10	P70366	STEROID RECEPTOR COACT	5.12e+00
11	000150	71.4%	1441	2	000150	STEROID RECEPTOR COACT	5.12e+00
12	P70365	71.4%	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	5.12e+00
13	058811	69.8%	99	9	058811	HYPOTHETICAL 11.5 KD P	9.10e+00
14	019956	69.8%	407	3	019956	STIMILARITY TO S. CERVI	9.10e+00
15	031012	69.8%	448	9	031012	ORF51X5 PROTEIN.	9.10e+00
16	031210	69.8%	821	9	031210	GLYCOGEN PHOSPHORYLASE	1.60e+01
17	P96578	68.3%	167	9	P96578	YDAE PROTEIN.	1.60e+01
18	018251	68.3%	199	3	018251	Y57G11C.25	1.60e+01
19	P73618	68.3%	225	9	P73618	DEOXRIBOSE- PHOSPHATE	1.60e+01

Thu Jul 30 13:38:02 1998

US-08-817-547A-2.rsp

Page 2

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CCM 1904;
RA BRINGEL F.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: ATP + N-ACETYL-L-GLUTAMATE =
CC ADP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.
DR EMBL; X99978; E284231; -.
KW TRANSFERASE.
SQ SEQUENCE 248 AA; 26580 MW; 3E945D79 CRC32;

Query Match 76.2%; Score 48; DB 9; Length 248;
Best Local Similarity 44.4%; Pred. No. 8.60e-01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Caps 0;

DB 125 AVNOYQOLMQ 133
QY 1 SVSEIQLMH 9

Search completed: Thu Jul 30 09:59:02 1998
Job time : 16 secs.
```

M I S E R I E
(TM)

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Msrch_p protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:02:44 1998; Maspar time 2.60 Seconds
47.195 Million cell updates/sec

bular output not generated.

Title: >US-08-817-547A-3
Description: (1-8) from US08817547A.pep
Perfect Score: 54
Sequence: 1 SVSEIQLM 8

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.998; Variance 50.414; scale 0.298

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description	Pred. No.
1	54	100.0	17 18	R94192	Human parathyroid hor	2.22e+01
2	54	100.0	34 20	R99978	Human parathyroid hor	2.22e+01
3	54	100.0	34 18	W01610	Parathyroid hormone a	2.22e+01
4	54	100.0	34 7	R43361	Human parathyroid hor	2.22e+01
5	54	100.0	34 7	R43360	Human parathyroid hor	2.22e+01
6	54	100.0	34 23	W24276	Parathyroid hormone (2.22e+01
7	54	100.0	34 23	W08130	Human PTH derivative,	2.22e+01
8	54	100.0	34 23	W08131	Human PTH derivative,	2.22e+01
9	54	100.0	34 23	W24273	Wild type parathyroid	2.22e+01
10	54	100.0	34 8	R41560	[His27]hPTH (1-34).	2.22e+01
11	54	100.0	34 8	R41559	[His27]hPTH (1-34).	2.22e+01
12	54	100.0	34 22	W17954	Human parathyroid hor	2.22e+01
13	54	100.0	34 22	W17955	Human parathyroid hor	2.22e+01
14	54	100.0	34 7	R43359	Human parathyroid hor	2.22e+01
15	54	100.0	34 7	R43357	Human parathyroid hor	2.22e+01
16	54	100.0	34 18	R88829	Human parathyroid hor	2.22e+01
17	54	100.0	34 20	W14312	Cyclic parathyroid ho	2.22e+01
18	54	100.0	34 20	R99981	Porcine parathyroid h	2.22e+01
19	54	100.0	34 8	R41565	[Arg16, Gln27]hPTH (1	2.22e+01

20	54	100.0	34 8	R41552	[Glu16]hPTH (1-34).	2.22e+01
21	54	100.0	34 9	R58189	[F23,H25,H26,L27,I28,	2.22e+01
22	54	100.0	34 22	W17952	Human parathyroid hor	2.22e+01
23	54	100.0	34 7	R43368	Human parathyroid hor	2.22e+01
24	54	100.0	34 23	W08114	Human PTH derivative,	2.22e+01
25	54	100.0	34 22	W19994	Cyclised human parath	2.22e+01
26	54	100.0	34 9	R58181	[Thr33, Ala34]-hPTH(1	2.22e+01
27	54	100.0	34 7	R43356	Human parathyroid hor	2.22e+01
28	54	100.0	34 8	R41568	Human parathyroid hor	2.22e+01
29	54	100.0	34 8	R58275	[Lys15-16 His27]hPTH	2.22e+01
30	54	100.0	36 9	R58276	[Ala16]-hPTH(1-36)-NH	2.22e+01
31	54	100.0	36 9	R58278	[Met(02)]hPTH(1-36)	2.22e+01
32	54	100.0	36 9	R58238	[D-Asp30]-hPTH(1-36)-	2.22e+01
33	54	100.0	36 9	R58237	[NMePhe34]-hPTH(1-36)-	2.22e+01
34	54	100.0	36 9	R58249	[D-Ser1]-hPTH(1-36)-N	2.22e+01
35	54	100.0	36 9	R58188	[Phe23]-hPTH(1-36)-NH	2.22e+01
36	54	100.0	37 9	R58245	[Pro0]-hPTH(1-36)-NH2	2.22e+01
37	54	100.0	38 9	R58097	[Thr13]-hPTH(1-38)-OH	2.22e+01
38	54	100.0	38 9	R58143	[Gln21]-hPTH(1-38)-OH	2.22e+01
39	54	100.0	38 9	R58114	[Val115]-hPTH(1-38)-OH	2.22e+01
40	54	100.0	44 26	P30015	Human parathyroid hor	2.22e+01
41	54	100.0	47 25	W21946	Fusion protein compri	2.22e+01
42	54	100.0	84 27	W25687	Human parathyroid hor	2.22e+01
43	54	100.0	84 8	R42076	Stability-enhanced hu	2.22e+01
44	54	100.0	84 25	W29420	Human parathyroid hor	2.22e+01
45	54	100.0	84 4	R23500	Porcine parathyroid h	2.22e+01

ALIGNMENTS

RESULT 1
ID R94192 standard; peptide; 17 AA.
AC R94192;
DT 07-OCT-1996 (first entry)
DE Human parathyroid hormone amino acids 1-17.
KW Chitosan; squid; chitin; human parathyroid hormone; hPTH; vaccine;
KM Immune response; biodegradable; synthesis method; support.
OS Synthetic.
PN CA2126132-A.
PD 18-DEC-1995.
PE 17-JUN-1994; 126132.
PF 17-JUN-1994; CA-126132.
PR 17-JUN-1994; CA-126132.
PA (NEUG) NEUGEBAUER W.
PI Brzelnski R, Neugebauer W, Willick GE;
DR WPI; 96-151747/16.
PT Peptide synthesis by sequentially attaching desired amino acids to
PT chitosan support - the peptide-chitosan complexes are useful in
PT generating predictable and controlled immune response
PS Example 4; Page 14; 24pp; English.
CC R94191 is a peptide corresp. to amino acids 44-68 of human parathyroid
CC hormone (hPTH) that was synthesised on a chitosan support. Chitosan
CC is derived from chitin by deacetylation, the chitosan used for the
CC support was derived from squid pen chitin. Bifunctional cleavable
CC linker molecules are attached to the free amino groups of chitosan
CC and the amino acids for the protein to be synthesised are attached
CC via the linker molecules. Peptide-chitosan complexes can be used
CC directly for injection into an animal to raise an immune response as
CC chitosan is biodegradable and exhibits little or no antigenic
CC properties. The linker molecule has a third functional gp. to which
CC an immunostimulatory structure may be attached. The method may further
CC comprise capping any remaining free amino gps. on the chitosan after
CC the first amino acid and/or linker molecule has been attached.
SQ Sequence 17 AA;

Query Match 100.0%; Score 54; DB 18; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.22e+01; Mismatches 0; Gaps 0;

Matches 8; Conservative 0; Indels 0; Gaps 0;
Db 1 svseiqm 8
1 svseiqm 8

RESULT 2

ID R99978 standard; peptide: 34 AA.

AC R99978;

DT 30-APR-1997 (first entry)

DE Human parathyroid hormone peptide fragment (1-34).

KW cyclic parathyroid hormone fragment; calcium-regulating activity; osteoporosis; inhibit proliferation; epidermal cell; psoriasis;

KW Improved half life; calcium retention; bone.

OS Synthetic.

PN DE19508672-A1.

PD 12-SEP-1996.

PF 10-MAR-1995; 008672.

PR 10-MAR-1995; DE-008672.

PA (BOE) BOEHRINGER MANNHEIM GMBH.

PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;

DR MPI; 96-413519/42.

PT Cyclic parathyroid hormone fragments with lactam bridge - have good in vivo half life and are useful for treating osteoporosis and preventing epidermal cell proliferation

Disclosure; Page 9; 14pp; German.

New cyclic parathyroid hormone fragments (CPTH) have the amino acid sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at the N-terminus, and are cyclised between positions 13 and 17. One of these positions is occupied by L- or D- Orn or Lys, and the other by L- or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for treating osteoporosis and inhibit proliferation of epidermal cells (for treating psoriasis). The CPTH have an improved half life in vivo than known PTH fragments, increased mitogenicity and DNA-synthesising capacity, reduced catabolic, calcium-mobilising activity and increased activity for calcium retention and incorporation into bone. The present sequence is that of human PTH peptide fragment (1-34).

SQ Sequence 34 AA;

Query Match 100.0%; Score 54; DB 20; Length 34;

Best local Similarity 100.0%; Pred. No. 2.22e+01;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 svseqlm 8

QY 1 SVSEQLM 8

Search completed: Thu Jul 30 10:03:01 1998
 Job time : 17 secs.

Thu Jul 30 13:38:11 1998

US-08-817-547A-3.rpt

17-28 #region helix (right hand alpha)
SUMMARY #length 37 #molecular-weight 4401 #checksum 3791

Query Match 100.0%; Score 54; DB 5; length 37;
Best Local Similarity 100.0%; Pred. No. 6.75e-02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Db 1 SVSEIQLM 8
|||
QY 1 SVSEIQLM 8

Search completed: Thu Jul 30 10:02:26 1998
Job time : 28 secs.

W E S T E R N
(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:00:33 1998; MasPar time 2.09 Seconds
Abular output not generated. 95.854 Million cell updates/sec

Title: >US-08-817-547A-3
Description: (1-8) from US08817547A.pep
Perfect Score: 54
Sequence: 1 SVSEIQLM 8

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 21.952; Variance 19.669; scale 1.116

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	54	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	4.02e-03
2	54	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.02e-03
3	52	96.3	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.58e-02
4	49	90.7	119	1	PTHY_CHICK PARATHYROID HORMONE PR	1.16e-01
5	47	87.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.17e-01
6	45	83.3	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.45e+00
7	43	79.6	1134	1	TYROSINE-PROTEIN KINAS	4.80e+00
8	43	79.6	1134	1	TYROSINE-PROTEIN KINAS	4.80e+00
9	41	75.9	259	1	Y224_METUA HYPOTHETICAL PROTEIN M	1.52e+01
10	41	75.9	312	1	Y085_MYCPN HYPOTHETICAL PROTEIN M	1.52e+01
11	41	75.9	369	1	PROB_CORGL GLUTAMATE 5-KINASE (EC	1.52e+01
12	41	75.9	441	1	CG22_ANTMA G2/MITOTIC-SPECIFIC CY	1.52e+01
13	41	75.9	481	1	KRCB_RAT RAC-BETA SERINE/THREON	1.52e+01
14	41	75.9	481	1	KRCB_HUMAN RAC-BETA SERINE/THREON	1.52e+01
15	41	75.9	591	1	FLOI_HUMAN PLACENTAL FOLATE TRANS	1.52e+01
16	41	75.9	605	1	VEL_HPYO9 REPLICATION PROTEIN E1	1.52e+01
17	41	75.9	675	1	VPS5_YEAST VACUOLAR PROTEIN SORTI	1.52e+01
18	41	75.9	835	1	VIRL_AGR16 LIMITED HOST RANGE (LH	1.52e+01
19	41	75.9	896	1	APCE_SYN4 PHYCOBILISOME 100.5 KD	2.66e+01
20	40	74.1	306	1	RIR2_ZYVD RIBONUCLEOSIDE-DIPHOS	2.66e+01
21	40	74.1	341	1	YSX3_CAEEL HYPOTHETICAL 39.0 KD P	2.66e+01
22	40	74.1	870	1	COPG_CAEEL PROBABLE COATOWER GAMM	2.66e+01
23	40	74.1	1061	1	TRC4_ECOLI DNA PRIMASE TRAC (EC 2	2.66e+01

RESULT	ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	24	40	74.1	1150	1	YIC6_YEAST HYPOTHETICAL 133.0 KD
DT	25	40	74.1	1487	1	MD53_YEAST MD53 PROTEIN (MCK1 DOS
DT	26	40	74.1	3124	1	CA1C_CHICK COLLAGEN ALPHA 1(XII)
DT	27	39	72.2	106	1	RPE_RHOCA RIBULOSE-PHOSPHATE 3-E
DT	28	39	72.2	207	1	RR4_CHLEL CHLOROBLAST 30S RIBOSO
DT	29	39	72.2	220	1	CRG2_RAT GLUTATHIONE S-TRANSFER
DT	30	39	72.2	248	1	LEP3_BACSU TYPE 4 PREPILIN-LIKE P
DT	31	39	72.2	455	1	DCOR_CRIGR ORNITHINE DECARBOXYLAS
DT	32	39	72.2	455	1	DCOR_CRIGR ORNITHINE DECARBOXYLAS
DT	33	39	72.2	461	1	DCOR_MUSPA ORNITHINE DECARBOXYLAS
DT	34	39	72.2	461	1	DCOR_MOUSE ORNITHINE DECARBOXYLAS
DT	35	39	72.2	474	1	MEC3_YEAST CHECKPOINT PROTEIN MEC
DT	36	39	72.2	503	1	HSP1_MOUSE HEAT SHOCK FACTOR PROT
DT	37	39	72.2	525	1	SP1_RARFA SERINE PROTEINASE I PREC
DT	38	39	72.2	529	1	HSP1_HUMAN HEAT SHOCK FACTOR PROT
DT	39	39	72.2	567	1	CYDC_BACSU TRANSPORT ATP-BINDING
DT	40	39	72.2	626	1	TESTIS-SPECIFIC PROTEIN
DT	41	39	72.2	628	1	TESTIS-SPECIFIC PROTEIN
DT	42	39	72.2	1116	1	PROB_HETCA DNA-DIRECTED RNA POLYM
DT	43	39	72.2	1436	1	WC11_BOVIN ANTIGEN WC1.1.
DT	44	39	72.2	1827	1	CUT1_SCHPO CUT1 PROTEIN.
DT	45	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	46	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	47	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	48	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	49	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	50	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	51	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	52	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	53	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	54	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	55	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	56	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	57	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	58	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	59	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	60	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	61	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	62	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	63	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	64	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	65	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	66	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	67	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	68	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	69	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	70	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	71	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	72	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	73	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	74	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	75	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	76	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	77	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	78	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	79	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	80	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	81	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	82	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	83	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	84	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	85	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	86	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	87	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	88	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	89	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	90	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	91	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	92	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	93	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	94	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	95	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	96	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	97	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	98	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	99	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	100	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	101	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	102	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	103	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	104	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	105	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	106	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	107	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	108	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	109	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	110	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	111	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	112	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	113	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	114	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	115	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	116	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	117	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	118	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	119	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	120	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	121	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	122	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	123	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	124	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	125	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	126	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	127	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	128	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	129	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	130	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	131	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	132	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	133	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	134	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	135	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	136	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	137	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	138	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	139	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	140	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	141	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	142	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	143	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	144	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	145	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	146	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	147	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	148	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	149	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	150	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	151	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	152	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	153	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	154	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	155	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	156	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	157	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	158	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	159	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	160	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	161	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	162	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	163	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	164	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	165	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	166	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	167	39	72.2	2109	1	RRLP_VSVS3 RNA POLYMERASE BETA SU
DT	168	39	72.2	2109	1	RRL

Db 18 lrkklqdvh 26
 |||||
 QY 1 LRRKLDVH 9

RESULT 2

ID R62432 standard; peptide; 34 AA.
 AC R62432:
 DT 31-JUL-1995 (first entry)
 DE Accelerator peptide basic region peptide, P-8.
 KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
 KW periodontal tissue; regeneration; periodontitis; periodontal pocket;
 OS down growth; epithelium; fibre adhesion; cement.
 OS Synthetic.
 PN J06234653-A.
 PD 23-AUG-1994.
 PF 10-FEB-1993; 045998.
 PR 10-FEB-1993; JP-045998.
 (SUNZ) SUNSTAR CHEM IND CO LTD.
 WPI: 95-157631/21.
 Accelerator for regenerating periodontal tissue - comprises
 PT peptide having 3-34 aminoacid residues having connected basic
 PT aminoacid residues
 PS Disclosure: Page 3: 7pp. Japanese.
 CC The sequences in R62423-36 are peptide fragments of an accelerator
 CC protein which contain at least two basic amino acids. The accelerator
 CC also comprises a cell growth factor. The accelerator may be used to
 CC accelerate the growth of periodontal tissue regeneration. The
 CC accelerator is applied by opening the gingiva, treating the tissue
 CC destroyed by periodontitis and applying the accelerator in the
 CC periodontal pocket. The accelerator reduces the down growth of the
 CC epithelium and accelerates fibre adhesion and regenerates cement.
 SQ Sequence 34 AA;

Query Match

Best Local Similarity 100.0%; Score 68; DB 26; Length 34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 lrkklqdvh 32
 |||||
 QY 1 LRRKLDVH 9

Search completed: Thu Jul 30 11:15:26 1998
 Job time : 17 secs.

NWSEIPI (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:14:22 1998; Maspar time 3.17 Seconds
Tabular output not generated. 103.833 Million cell updates/sec

Title: >US-08-817-547A-32
Description: (1-9) from US08817547A.pep
Perfect Score: 68
Sequence: 1 LRKKLDVH 9

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:n1r13d

Statistics: Mean 23.542; Variance 35.708; scale 0.659

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	68	100.0	34	5	12WG parathyroid hormone 4	1.61e-02
2	68	100.0	34	5	12WF parathyroid hormone 4	1.61e-02
3	68	100.0	34	5	12WH cyclic parathyroid ho	1.61e-02
4	68	100.0	34	5	12WE parathyroid hormone	1.61e-02
5	68	100.0	34	5	12MA parathyroid hormone	1.61e-02
6	68	100.0	35	5	12MD parathyroid hormone	1.61e-02
7	68	100.0	36	5	12WB parathyroid hormone	1.61e-02
8	68	100.0	37	5	12WC parathyroid hormone	1.61e-02
9	68	100.0	37	5	12WP parathyroid hormone	1.61e-02
10	68	100.0	115	1	PMBO parathyroid hormone	1.61e-02
11	68	100.0	115	1	UC4202 parathyroid hormone	1.61e-02
12	68	100.0	115	1	PTHU parathyroid hormone	1.61e-02
13	68	100.0	115	1	A05091 parathyroid hormone	1.61e-02
14	68	100.0	115	1	151851 parathyroid hormone	1.61e-02
15	58	83.3	105	2	A34937 parathyroid hormone	6.51e+00
16	54	79.4	119	2	15894 parathyroid hormone	6.51e+00
17	54	79.4	421	5	15894 parathyroid hormone	6.51e+00
18	54	79.4	421	5	15894 parathyroid hormone	6.51e+00
19	54	79.4	421	5	15894 parathyroid hormone	6.51e+00
20	54	79.4	421	5	15894 parathyroid hormone	6.51e+00
21	54	79.4	421	5	15894 parathyroid hormone	6.51e+00
22	54	79.4	421	5	15894 parathyroid hormone	6.51e+00
23	54	79.4	421	5	15894 parathyroid hormone	6.51e+00

Result	ENTRY	ENTRY TITLE	12WG	#type complete	ALIGNMENTS
24	54	79.4	421	5	15894
25	53	77.9	348	2	545850
26	52	76.5	878	2	520486
27	52	76.5	879	2	522028
28	52	76.5	2475	2	535307
29	51	75.0	257	2	53306
30	51	75.0	317	2	545708
31	51	75.0	412	2	577524
32	50	73.5	437	2	507537
33	50	73.5	437	2	564113
34	50	73.5	569	2	562851
35	50	73.5	586	2	544850
36	50	73.5	621	2	510450
37	50	73.5	1938	2	505421
38	50	73.5	1972	2	505420
39	50	73.5	4725	1	544357
40	49	72.1	215	2	535640
41	49	72.1	630	2	564302
42	48	70.6	154	2	503242
43	48	70.6	229	2	570073
44	48	70.6	444	2	509681
45	48	70.6	1126	2	504716

RESULT 1
ENTRY 12WG
TITLE parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -
synthetic
ALTERNATE_NAMES n-succinyl-hpeth(4-37)
PDB_TITLE succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM #formal_name synthetic
REFERENCE A67743
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WG
REFERENCE TN003319
#authors Marx, U.C.
#book In Strukturen Verschiedener Parathormonfragmente in Loesung,
pp.0, Bayreuth: University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
KEYWORDS Determination: NMR
FEATURES disease mutation: hormone; signal
2-9
15-25
SUMMARY #region helix (right hand alpha) \
#length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 68; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.61e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 21 LRKKLDVH 29
QY 1 LRKKLDVH 9
RESULT 2
ENTRY 12WF
TITLE parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -
synthetic
ALTERNATE_NAMES n-acetyl-hpeth(4-37)
PDB_TITLE structure of n-terminal acetylated human parathyroid hormone,
NMR, 10 structures
ORGANISM #formal_name synthetic
REFERENCE A67742
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WF
REFERENCE TN003318
#authors Marx, U.C.
#book In Strukturen Verschiedener Parathormonfragmente in Loesung,

PP: 0, Bayreuth : University of Bayreuth (Thesis), 1996
 COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 3-6 #region helix (right hand alpha)\
 14-27 #region helix (right hand alpha)
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 68; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.61e-02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 21 LRRKLQDVH 29
 1 LRRKLQDVH 9

Search completed: Thu Jul 30 11:14:51 1998
 Time : 29 secs.

W O R L D
(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:13:17 1998; MasPar time 2.13 Seconds
Tabular output not generated. 105.752 Million cell updates/sec

Title: >US-08-817-547A-32
Description: (1-9) from US08817547A.pep
Perfect Score: 68
Sequence: 1 LRRKLODVH 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 24.742; Variance 29.653; scale 0.834

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	68	100.0	115	1	PTHY_BOVIN	8.13e-04
2	68	100.0	115	1	PTHY_BOVIN	8.13e-04
3	68	100.0	115	1	PTHY_CANFA	8.13e-04
4	68	100.0	115	1	PTHY_PIG	8.13e-04
5	68	100.0	115	1	PTHY_RAT	8.13e-04
6	68	100.0	115	1	PTHY_HUMAN	8.13e-04
7	68	100.0	115	1	PTHY_CHICK	8.13e-04
8	68	100.0	115	1	PTHY_CHICK	8.13e-04
9	68	100.0	115	1	PTHY_CHICK	8.13e-04
10	68	100.0	115	1	PTHY_CHICK	8.13e-04
11	68	100.0	115	1	PTHY_CHICK	8.13e-04
12	68	100.0	115	1	PTHY_CHICK	8.13e-04
13	68	100.0	115	1	PTHY_CHICK	8.13e-04
14	68	100.0	115	1	PTHY_CHICK	8.13e-04
15	68	100.0	115	1	PTHY_CHICK	8.13e-04
16	68	100.0	115	1	PTHY_CHICK	8.13e-04
17	68	100.0	115	1	PTHY_CHICK	8.13e-04
18	68	100.0	115	1	PTHY_CHICK	8.13e-04
19	68	100.0	115	1	PTHY_CHICK	8.13e-04
20	68	100.0	115	1	PTHY_CHICK	8.13e-04
21	68	100.0	115	1	PTHY_CHICK	8.13e-04
22	68	100.0	115	1	PTHY_CHICK	8.13e-04
23	68	100.0	115	1	PTHY_CHICK	8.13e-04

RESULT	ID	PTHY_BOVIN	STANDARD	PRT	115 AA.	ALIGNMENTS
AC	21-JUL-1986	(REL. 01, CREATED)				
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
OC	EURARCTOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; ARTIODACTYLA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 80056617.					
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,					
RA	POTTS J.T. JR., RICH A.,					
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 82037785.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RA	GENE 28:319-329(1984).					
RN	[5]					
RP	SEQUENCE OF 26-115.					
RX	MEDLINE: 74142666.					
RA	HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,					
RA	COHN D.V.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).					
RN	[6]					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE: 71076162.					
RA	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.T., DAWSON B.F.,					
RA	AURBACH G.D., POTTS J.T. JR.;					
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).					
RN	[7]					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE: 71063634.					

Search completed: Thu Jul 30 11:13:23 1998
Job time : 6 secs.

RA BREWER H.B. JR., RONAN R.,
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NITALL H.D., SAUER R.,
RA DEFLOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; V00106; G85; -.
DR EMBL; J00023; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18249; ALT_SRO.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; M25082; G163647; -.
DR EMBL; M25082; G163645; -.
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
OC HORMONE; SIGNAL.
FT PROPEP 1 25
FT CHAIN 26 31
FT CONFLICT 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;

Query Match 100.0%; Score 68; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.13e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LKKKLQDVH 63
QY 1 LKKKLQDVH 9

RESULT 2
ID PTH_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE-PARATHYROID;
CC MEDLINE; 95369696.
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
RA DEVILLE J.W., CAPEN C.C.;
RL GENE 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; U15662; G55816; -.
DR PROSITE; PS00335; PARATHYROID; 1.
DR KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12957 MM; 16E0DEBC CRC32;

Query Match 100.0%; Score 68; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.13e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LKKKLQDVH 63
QY 1 LKKKLQDVH 9

WORLDWIDE
(TM)

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mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:13:41 1998; MasPar time 3.75 Seconds
Tabular output not generated. 101.012 Million cell updates/sec

Title: >US-08-817-547A-32
Description: (1-9) from US08817547A.pep
Perfect Score: 68
Sequence: 1 LRRKLDVH 9

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_prodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 23.769; Variance 29.317; scale 0.811

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	58	85.3	105	10	063473	PARATHYROID HORMONE (F	2.16e+01
2	54	79.4	735	8	017750	C06G3.9 PROTEIN	1.57e+00
3	53	77.9	398	8	004471	SIMILAR TO SACHAROMYC	2.54e+00
4	52	76.5	929	9	032491	PUTATIVE N6-ADEININE S	4.08e+00
5	52	76.5	1312	2	092878	RAD50.	4.08e+00
6	52	76.5	2475	11	008358	POLYPROTEIN PP220.	6.52e+00
7	51	75.0	242	8	P93468	MADS-BOX FAMILY TRANSC	6.52e+00
8	51	75.0	242	8	040970	PUTATIVE MADS-BOX FAMI	6.52e+00
9	51	75.0	257	8	040700	BOX PROTEIN.	6.52e+00
10	51	75.0	317	4	P79328	MELANOCYTE STIMULATING	6.52e+00
11	51	75.0	317	4	019037	MCL-R PROTEIN.	6.52e+00
12	51	75.0	733	3	024250	TARTAN PROTEIN PRECURS	6.52e+00
13	51	75.0	1200	9	P73340	CHROMOSOME SEGREGATION	6.52e+00
14	50	73.5	379	10	063338	MYOSIN HEAVY CHAIN (AA	1.04e+01
15	50	73.5	334	3	017970	CL4C10.1.	1.04e+01
16	50	73.5	621	10	063339	MYOSIN HEAVY CHAIN 21	1.04e+01
17	50	73.5	1938	10	008639	MYOSIN.	1.04e+01
18	50	73.5	1972	10	008638	MYOSIN.	1.04e+01
19	49	72.1	400	3	026648	TEKTIN B1.	1.64e+01
20	49	72.1	991	2	Q14844	MYOSIN LIGHT CHAIN KIN	1.64e+01

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	063473.			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-THYROID, AND PARATHYROID;			
RA	SCHNEIDER H.T., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -.			
FT	NON_TER			
SEQ	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;			

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	063473.			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-THYROID, AND PARATHYROID;			
RA	SCHNEIDER H.T., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -.			
FT	NON_TER			
SEQ	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;			

Query Match 85.3%; Score 58; DB 10; Length 105;
Best Local Similarity 88.9%; Pred. No. 2.16e+01;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB	45 LRRKLDVH 53
QY	1 LRRKLDVH 9
RESULT	2
ID	017750.
AC	017750.
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE	C06G3.9 PROTEIN.
GN	C06G3.9.
OS	CANORHABDITIS ELEGANS.
OC	EUDAROTA; METAZOA; ACCELLOMATES; NEMATODA; SECCERNENTIA; RHABDITIDA.
OC	EUDAROTA; METAZOA; ACCELLOMATES; NEMATODA; SECCERNENTIA; RHABDITIDA.
RP	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL N2;
RA	LARREILLE P., STELIVES L.;
RL	SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBSJ DATA BANKS.

Thu Jul 30 13:38:14 1998

US-08-817-547A-32.ispt






Page 2

DR EMBL: D61947: G1397274: -
SQ SEQUENCE 735 AA: 81001 MW: 84A565C0 CRC32:

Query Match 79.48; Score 54; DB 3; Length 735;
Best Local Similarity 66.78; Pred. No. 1.57e+00;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 486 LRRKVDIO 494
QY 1 LRRKLDVH 9

Search completed: Thu Jul 30 11:14:05 1998
Job time : 24 secs.

Db 18 LKKLQDV 25
 |||||
 QY 1 LKKLQDV 8

RESULT 2
 ID R62432 standard; peptide; 34 AA.

AC R62432;

DT 31-JUL-1995 (first entry)

DE Accelerator peptide basic region peptide, P-8.

KW Accelerator: basic amino acid; cell growth factor; growth; gingiva;
 periodontal tissue; regeneration; periodontitis; periodontal pocket;
 down growth; epithelium; fibre adhesion; cement.

KW Synthetic.

OS J06234653-A.

PN 23-AUG-1994.

PD 10-FEB-1993; 045998.

PF 10-FEB-1993; JP-045998.

PR (SUNZ) SUNSTAR CHEM IND CO LTD.

WPI: 95-157631/21.

Accelerator for regenerating periodontal tissue - comprises

peptide having 3-34 aminoacid residues having connected basic

aminoacid residues

PS Disclosure: Page 3; 7pp; Japanese.

CC The sequences in R62425-36 are peptide fragments of an accelerator

protein which contain at least two basic amino acids. The accelerator

also comprises a cell growth factor. The accelerator may be used to

accelerate the growth of periodontal tissue regeneration. The

accelerator is applied by opening the gingiva, treating the tissue

destroyed by periodontitis and applying the accelerator in the

periodontal pocket. The accelerator reduces the down growth of the

epithelium and accelerates fibre adhesion and regenerates cement.

CC Sequence 34 AA;

SQ

Query Match 100.0%; Score 59; DB 26; Length 34;

Best Local Similarity 100.0%; Pred. No. 9.92e+00; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0;

Db 24 LKKLQDV 31
 |||||

QY 1 LKKLQDV 8

Search completed: Thu Jul 30 11:17:51 1998
 Job time : 15 secs.

M O S E R
(TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:16:07 1998; Maspar time 3.11 Seconds
Tabular output not generated. 93.824 Million cell updates/sec

Title: >US-08-817-547A-33
Description: (1-8) from US08817547A.dep
Perfect Score: 59
Sequence: 1 LRRKLODV 8

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 3653193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 22.968; Variance 34.253; scale 0.671

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	ID	Description	Pred. No.
1	59	100.0	34	parathyroid hormone 4	4.79e-01
2	59	100.0	34	parathyroid hormone 4	4.79e-01
3	59	100.0	34	parathyroid hormone 4	4.79e-01
4	59	100.0	34	parathyroid hormone 4	4.79e-01
5	59	100.0	34	parathyroid hormone 4	4.79e-01
6	59	100.0	34	parathyroid hormone 4	4.79e-01
7	59	100.0	34	parathyroid hormone 4	4.79e-01
8	59	100.0	34	parathyroid hormone 4	4.79e-01
9	59	100.0	34	parathyroid hormone 4	4.79e-01
10	59	100.0	34	parathyroid hormone 4	4.79e-01
11	59	100.0	34	parathyroid hormone 4	4.79e-01
12	59	100.0	34	parathyroid hormone 4	4.79e-01
13	59	100.0	34	parathyroid hormone 4	4.79e-01
14	59	100.0	34	parathyroid hormone 4	4.79e-01
15	59	100.0	34	parathyroid hormone 4	4.79e-01
16	59	100.0	34	parathyroid hormone 4	4.79e-01
17	59	100.0	34	parathyroid hormone 4	4.79e-01
18	59	100.0	34	parathyroid hormone 4	4.79e-01
19	59	100.0	34	parathyroid hormone 4	4.79e-01
20	59	100.0	34	parathyroid hormone 4	4.79e-01
21	59	100.0	34	parathyroid hormone 4	4.79e-01
22	59	100.0	34	parathyroid hormone 4	4.79e-01
23	59	100.0	34	parathyroid hormone 4	4.79e-01

Query	Match	Length	ID	Description	Pred. No.
1	59	100.0	34	parathyroid hormone 4	4.79e-01
2	59	100.0	34	parathyroid hormone 4	4.79e-01
3	59	100.0	34	parathyroid hormone 4	4.79e-01
4	59	100.0	34	parathyroid hormone 4	4.79e-01
5	59	100.0	34	parathyroid hormone 4	4.79e-01
6	59	100.0	34	parathyroid hormone 4	4.79e-01
7	59	100.0	34	parathyroid hormone 4	4.79e-01
8	59	100.0	34	parathyroid hormone 4	4.79e-01
9	59	100.0	34	parathyroid hormone 4	4.79e-01
10	59	100.0	34	parathyroid hormone 4	4.79e-01
11	59	100.0	34	parathyroid hormone 4	4.79e-01
12	59	100.0	34	parathyroid hormone 4	4.79e-01
13	59	100.0	34	parathyroid hormone 4	4.79e-01
14	59	100.0	34	parathyroid hormone 4	4.79e-01
15	59	100.0	34	parathyroid hormone 4	4.79e-01
16	59	100.0	34	parathyroid hormone 4	4.79e-01
17	59	100.0	34	parathyroid hormone 4	4.79e-01
18	59	100.0	34	parathyroid hormone 4	4.79e-01
19	59	100.0	34	parathyroid hormone 4	4.79e-01
20	59	100.0	34	parathyroid hormone 4	4.79e-01
21	59	100.0	34	parathyroid hormone 4	4.79e-01
22	59	100.0	34	parathyroid hormone 4	4.79e-01
23	59	100.0	34	parathyroid hormone 4	4.79e-01

ALIGNMENTS

Query	Match	Length	ID	Description	Pred. No.
1	59	100.0	34	parathyroid hormone 4	4.79e-01
2	59	100.0	34	parathyroid hormone 4	4.79e-01
3	59	100.0	34	parathyroid hormone 4	4.79e-01
4	59	100.0	34	parathyroid hormone 4	4.79e-01
5	59	100.0	34	parathyroid hormone 4	4.79e-01
6	59	100.0	34	parathyroid hormone 4	4.79e-01
7	59	100.0	34	parathyroid hormone 4	4.79e-01
8	59	100.0	34	parathyroid hormone 4	4.79e-01
9	59	100.0	34	parathyroid hormone 4	4.79e-01
10	59	100.0	34	parathyroid hormone 4	4.79e-01
11	59	100.0	34	parathyroid hormone 4	4.79e-01
12	59	100.0	34	parathyroid hormone 4	4.79e-01
13	59	100.0	34	parathyroid hormone 4	4.79e-01
14	59	100.0	34	parathyroid hormone 4	4.79e-01
15	59	100.0	34	parathyroid hormone 4	4.79e-01
16	59	100.0	34	parathyroid hormone 4	4.79e-01
17	59	100.0	34	parathyroid hormone 4	4.79e-01
18	59	100.0	34	parathyroid hormone 4	4.79e-01
19	59	100.0	34	parathyroid hormone 4	4.79e-01
20	59	100.0	34	parathyroid hormone 4	4.79e-01
21	59	100.0	34	parathyroid hormone 4	4.79e-01
22	59	100.0	34	parathyroid hormone 4	4.79e-01
23	59	100.0	34	parathyroid hormone 4	4.79e-01

Thu Jul 30 13:38:15 1998

US-08-817-547A-33.rpr

Page 2

pp. 0, Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 59; DB 5; Length 34;
Best local Similarity 100.0%; Pred. No. 4.79e-01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 21 LRRKLDV 28
Qy 1 LRRKLDV 8

Search completed: Thu Jul 30 11:16:30 1998
Time : 23 secs.

WISCONSIN
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:15:44 1998; MasPar time 2.11 Seconds
Tabular output not generated. 95.235 Million cell updates/sec

Title: >US-08-817-547A-33
Description: (1-8) from US08817547A.pap
Perfect Score: 59
Sequence: 1 LRRKLDV 8

Scoring table: PAM 150
Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 24.101; Variance 28.427; scale 0.848

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	59	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.95e-02
2	59	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.95e-02
3	59	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.95e-02
4	59	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	4.95e-02
5	59	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	4.95e-02
6	51	86.4	310	1	SYNK_ARATH SYNTHAXIN-RELATED PROTE	2.83e+00
7	51	86.4	317	1	MSHR_BOVIN MELANOCYTE STIMULATING	2.83e+00
8	50	84.7	421	1	SYS_THETH SERYL-TRNA SYNTHETASE	4.56e+00
9	50	84.7	437	1	FOLC_HAEIN FOLYPOLYGLUTAMATE SYN	4.56e+00
10	50	84.7	586	1	YMG1_GABEL HYPOTHETICAL 65.8 KD P	4.56e+00
11	50	84.7	621	1	Y04E_MYCTU HYPOTHETICAL 69.2 KD P	4.56e+00
12	50	84.7	4725	1	DYHC_DICDI DYNENIN HEAVY CHAIN, CY	4.56e+00
13	49	83.1	209	1	VS10_ROTBS MINOR OUTER CAPSID PRO	7.30e+00
14	49	83.1	630	1	Y019_METJA HYPOTHETICAL PROTEIN M	7.30e+00
15	48	81.4	154	1	Y17K_SSV1 HYPOTHETICAL 17.8 KD P	1.16e+01
16	48	81.4	419	1	PEXA_PICPA PEROXISOME ASSEMBLY PR	1.16e+01
17	48	81.4	1126	1	PROB_SRIAC DNA-DIRECTED RNA POLYM	1.16e+01
18	47	79.7	100	1	Y191_ECOLI INSERTION ELEMENT IS91	1.83e+01
19	47	79.7	112	1	Y191_SHIDY INSERTION ELEMENT IS91	1.83e+01
20	46	78.0	100	1	RRL4_PORPU CHLOROPLAST 30S RIBOSO	2.86e+01
21	46	78.0	224	1	TCED_SALTY TRANSACRIPATIONAL RESUL	2.86e+01
22	46	78.0	229	1	YXDJ_BACSU HYPOTHETICAL 26.6 KD S	2.86e+01
23	46	78.0	326	1	YIEL_YEAST 36.7 KD PROTEIN IN CBR	2.86e+01

RESULT	ID	PTHY_BOVIN	STANDARD:	PTHY	115 AA.	ALIGNMENTS
AC	P01268:					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRLIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; ARTIODACTYLA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,					
RA	POTTS J.T. JR., RICH A.;					
RA	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).					
RL	[2]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RA	GENE 28:319-329(1984).					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RA	HAHLTON J.W., NYALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,					
RA	COHN D.V.;					
RA	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).					
RP	[6]					
RP	SEQUENCE OF 32-115.					
RA	MEDLINE: 71076162.					
RA	NYALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,					
RA	AURACH G.D., POTTS J.T. JR.;					
RA	HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1586-1588(1970).					
RP	[7]					
RP	SEQUENCE OF 32-115.					
RA	MEDLINE: 71063634.					

Thu Jul 30 13:38:15 1998

US-08-817-547A-33.rsp

Search completed: Thu Jul 30 11:15:51 1998
Job time : 7 secs.

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RA BREWER H.B. JR., ROMAN R.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).  
RN [8]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE: 71091588.  
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NALL H.D., SAUER R.,  
RA DEFTOS L.J., DAMSON B.F., HOGAN M.L., AURBACH G.D.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL: V00106; G85; -  
DR EMBL: J00023; G163641; -  
DR EMBL: J00024; G163643; -  
DR EMBL: J00024; E18249; ALT_SEQ.  
DR EMBL: J00024; E18250; ALT_INIT.  
DR EMBL: K01938; G163647; -  
DR EMBL: M25082; G163645; -  
DR PIR: A01534; PTBO.  
DR PIR: A24949; A24949.  
DR PROSITE: PS00335; PARATHYROID; 1.  
OC HORMONE: SIGNAL.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 115 PARATHYROID HORMONE.  
FT CONFLICT 106 106 V->G (IN REF. 4).  
SQ SEQUENCE 115 AA; 12960 MW; 673EA5F2 CRC32;  
  
Query Match 100.0%; Score 59; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4.95e-02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 55 LRRKLDV 62  
QY 1 LRRKLDV 8  
|||||  
  
RESULT 2  
ID PTH CANPA STANDARD; PRT; 115 AA.  
AC P52212;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).  
GN PTH.  
OS CANIS FAMILIARIS (DOG).  
OC EURAROTIA; METAROTIA; CHOROTATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; CARNIVORA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-PARATHYROID;  
RX MEDLINE: 95369696.  
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,  
RA DEWITTE J.W., CAPEN C.C.;  
RL GENE 160:241-243(1995).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL: U15662; G558916; -  
DR PROSITE: PS00335; PARATHYROID; 1.  
KW HORMONE: SIGNAL.  
FT SIGNAL 1 25 BY SIMILARITY.  
FT PROPEP 26 31 BY SIMILARITY.  
FT CHAIN 32 115 PARATHYROID HORMONE.  
SQ SEQUENCE 115 AA; 12957 MW; 16ED0BEC CRC32;  
  
Query Match 100.0%; Score 59; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4.95e-02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 55 LRRKLDV 62  
QY 1 LRRKLDV 8  
|||||
```


RC TISSUE-THYROID, AND PARATHYROID:
 RA SCHMELZER H.J., GROSS G., MAYER H.;
 RL ADV. GENE TECHNOL. 21:226-229(1984).
 DR EMBL; M54875; G601933; -.
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;

Query Match 88.1%; Score 52; DB 10; Length 105;
 Best local Similarity 100.0%; Pred. No. 2.21e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 45 LRKLIQD 51
 QY 1 LRKLIQD 7

Search completed: Thu Jul 30 11:17:18 1998
 Job time : 29 secs.

NWSEIT (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:20:11 1998; Maspar time 2.56 Seconds
41.969 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRRKLOD 7

Scoring table:

PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.842; Variance 50.654; scale 0.313

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	52	100.0	34 26	R62432	Accelerator peptide b	3.78e+01
2	52	100.0	34 2	R08300	Human parathyroid hor	3.78e+01
3	52	100.0	34 9	R58291	[Lys(For)26, Lys(For)	3.78e+01
4	52	100.0	34 9	R58232	[Lys32]-hPTH(1-34)-NH	3.78e+01
5	52	100.0	34 7	R34358	Human parathyroid hor	3.78e+01
6	52	100.0	34 22	W20009	Cyclised [Nle 8,18, T	3.78e+01
7	52	100.0	34 22	W20003	Cyclised [Nle 8,18, T	3.78e+01
8	52	100.0	34 22	W17963	Human PTH analogue (C	3.78e+01
9	52	100.0	35 14	R74453	Parathyroid hormone p	3.78e+01
10	52	100.0	35 14	R74486	Parathyroid hormone p	3.78e+01
11	52	100.0	35 14	R74440	Parathyroid hormone p	3.78e+01
12	52	100.0	35 14	R74439	Parathyroid hormone p	3.78e+01
13	52	100.0	35 14	R74485	Parathyroid hormone p	3.78e+01
14	52	100.0	35 14	R74397	Parathyroid hormone p	3.78e+01
15	52	100.0	36 9	R58191	[Ala34]-hPTH(1-36)-NH	3.78e+01
16	52	100.0	36 9	R58253	[4-aminobenzoic acid1	3.78e+01
17	52	100.0	36 9	R58237	[NMEpH34]-hPTH(1-36)	3.78e+01
18	52	100.0	36 9	R58238	[D-Asp30]-hPTH(1-36)-	3.78e+01
19	52	100.0	36 9	R58041	[Le,D10,K11,S14,I15,Q	3.78e+01

20	52	100.0	36 9	R58285	[Ala23]-hPTH(1-36)-NH	3.78e+01
21	52	100.0	36 9	R58069	Isopropyl- [Le,K]isopr	3.78e+01
22	52	100.0	36 9	R58227	[D-Gln29]-hPTH(1-36)-	3.78e+01
23	52	100.0	38 9	R58136	[Arg19]-hPTH(1-38)-OH	3.78e+01
24	52	100.0	38 9	R58108	[Arg14]-hPTH(1-38)-OH	3.78e+01
25	52	100.0	44 26	P30015	Human parathyroid hor	3.78e+01
26	52	100.0	44 27	W25687	Human parathyroid hor	3.78e+01
27	52	100.0	84 4	R23356	Bovine parathyroid ho	3.78e+01
28	52	100.0	84 4	R23357	Bovine parathyroid ho	3.78e+01
29	52	100.0	84 4	R23241	Human parathyroid hor	3.78e+01
30	52	100.0	84 4	R23242	Human parathyroid hor	3.78e+01
31	52	100.0	84 4	R23521	Bovine parathyroid ho	3.78e+01
32	52	100.0	84 4	R23453	Porcine parathyroid h	3.78e+01
33	52	100.0	84 4	R23243	Human parathyroid hor	3.78e+01
34	52	100.0	84 4	R23519	Bovine parathyroid hor	3.78e+01
35	52	100.0	84 4	R23434	Porcine parathyroid h	3.78e+01
36	52	100.0	84 4	R23273	Bovine parathyroid ho	3.78e+01
37	52	100.0	84 4	R21256	Human parathyroid hor	3.78e+01
38	52	100.0	84 4	R23368	Bovine parathyroid ho	3.78e+01
39	52	100.0	84 4	R23256	Bovine parathyroid ho	3.78e+01
40	52	100.0	84 4	R21251	Human parathyroid hor	3.78e+01
41	52	100.0	84 4	R23522	Human parathyroid hor	3.78e+01
42	52	100.0	84 4	R23547	Bovine parathyroid ho	3.78e+01
43	52	100.0	84 7	R24335	Bovine parathyroid ho	3.78e+01
44	52	100.0	84 4	R21239	Human parathyroid hor	3.78e+01
45	52	100.0	84 4	R23245	Human parathyroid hor	3.78e+01

ALIGNMENTS

RESULT 1
ID R62432 standard; peptide; 34 AA.
AC R62432;
DT 31-JUL-1995 (first entry)
DE Accelerator peptide basic region peptide, p-8.
KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW Periodontal tissue; regeneration; periodontitis; periodontal pocket;
KW down growth; epithelium; fibre adhesion; cement.
OS Synthetic.
PN J06234653-A.
PD 23-AUG-1994.
PF 10-FEB-1993.
PR 10-FEB-1993; JP-045998.
PA (SUNZ) SUNSTAR CHEM IND CO LTD.
DR WPI; 95-157631/21.
PT Accelerator for regenerating periodontal tissue - comprises
PT peptide having 3-34 aminoacid residues having connected basic
PT aminoacid residues.
PS Disclosure; Page 3; 7pp; Japanese.
CC The sequences in R62425-36 are peptide fragments of an accelerator
CC protein which contain at least two basic amino acids. The accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerate the growth of periodontal tissue regeneration. The
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC periodontal pocket. The accelerator reduces the down growth of the
CC epithelium and accelerates fibre adhesion and regenerates cement.
SQ Sequence 34 AA;
Query Match 100.0%; Score 52; DB 26; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.78e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 24 Lrrklqd 30
QY 1 LRRKLOD 7
RESULT 2
ID R08300 standard; protein; 34 AA.
AC R08300;
DT 18-FEB-1991 (first entry)
DE Human parathyroid hormone analogue, Tnp12 hPTH(7-34).

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.
OS Homo sapiens.
PN US4968669-A.
PD 06-NOV-1990.
PE 21-APR-1989; 341597.
PR 09-MAY-1988; US-191512.
PR 21-APR-1989; US-341597.
PA (MERI) MERCK & CO INC.
PI Rosenblatt M, Chocrov M;
DR WPI; 90-354642/47.
PT New para:thyroid hormone analogues - which inhibit hormone
PT activity by binding receptors while not producing second
PT messenger molecules
PS Claim 1; Column 8; 6pp; English.
CC Peptide analogues have high affinity for PTH cell surface receptors,
CC but do not stimulate production of secondary messenger molecules.
CC They may be used in inhibition of PTH action, and in diagnosis and
CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
CC Analogues may also be used in treatment of tumours and other cells
CC overproducing peptide hormone-like substances, and immune diseases
CC eg. allergic inflammation and hyperactive lymphocytes.
SQ Naturally occurring PTH levels may also be measured in vitro.
Sequence 34 AA;

Query Match 100.0%; Score 52; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.78e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKIqd 30
| | | | | | | |
QY 1 LKKKLOD 7

Search completed: Thu Jul 30 11:20:26 1998
Job time : 15 secs.

MIRAGE
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:19:28 1998; MasPar time 3.06 Seconds
Tabular output not generated. 83.440 Million cell updates/sec

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRKRLQD 7

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 21.946; Variance 32.007; scale 0.686

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	52	100.0	34	5	12WG parathyroid hormone 4	4.07e+00
2	52	100.0	34	5	12WF parathyroid hormone 4	4.07e+00
3	52	100.0	34	5	12RH cyclic parathyroid ho	4.07e+00
4	52	100.0	34	5	12WE parathyroid hormone	4.07e+00
5	52	100.0	34	5	12NA parathyroid hormone	4.07e+00
6	52	100.0	35	5	12WD parathyroid hormone	4.07e+00
7	52	100.0	36	5	12WB parathyroid hormone	4.07e+00
8	52	100.0	37	5	12HP parathyroid hormone	4.07e+00
9	52	100.0	37	5	12WC parathyroid hormone	4.07e+00
10	52	100.0	105	2	151851 parathyroid hormone	4.07e+00
11	52	100.0	115	2	UC4202 parathyroid hormone	4.07e+00
12	52	100.0	115	2	PRHU parathyroid hormone	4.07e+00
13	52	100.0	115	1	PRPG parathyroid hormone	4.07e+00
14	52	100.0	115	1	PRPG parathyroid hormone	4.07e+00
15	52	100.0	115	1	PRBO parathyroid hormone	4.07e+00
16	51	98.1	257	2	S53306 floral homeotic prote	6.22e+00
17	47	90.4	133	2	S75121 hypothetical protein	3.23e+01
18	47	90.4	154	2	S03242 hypothetical protein	3.23e+01
19	47	90.4	360	2	F69342 DNA primase homolog -	3.23e+01
20	46	88.5	100	2	S56508 hypothethical 11.6K pr	4.80e+01
21	46	88.5	122	2	D70083 hypothethical protein	4.80e+01
22	46	88.5	134	2	G64750 hypothethical protein	4.80e+01
23	46	88.5	224	2	A33861 Trans-activating tran	4.80e+01

24	46	88.5	447	2	B40896	Ca2+/calmodulin-depen	4.80e+01
25	46	88.5	509	2	S22339	steroid 17alpha-monoo	4.80e+01
26	46	88.5	637	1	WOEC2M	phosphotransferase sy	4.80e+01
27	46	88.5	745	2	S48019	kinesin-related prote	4.80e+01
28	46	88.5	754	2	S48020	kinesin-related prote	4.80e+01
29	46	88.5	793	2	S34830	kinesin-related prote	4.80e+01
30	46	88.5	806	2	E64221	phenylalanine--tRNA	4.80e+01
31	46	88.5	899	2	S51341	probable membrane pro	4.80e+01
32	46	88.5	1231	2	A54803	microtubule-associate	4.80e+01
33	46	88.5	2492	1	C44213	nonstructural polypor	4.80e+01
34	46	88.5	2492	1	A44213	nonstructural polypor	4.80e+01
35	46	88.5	2492	1	NMNTD	nonstructural polypor	4.80e+01
36	45	86.5	192	2	S22577	hypothetical protein	7.11e+01
37	45	86.5	258	2	S57793	homeotic protein A613	7.11e+01
38	45	86.5	275	2	JC5492	insertion element ISH	7.11e+01
39	45	86.5	355	2	S57398	NVVA protein - Emeric	7.11e+01
40	45	86.5	430	1	VEMSGF	glial fibrillary acid	7.11e+01
41	45	86.5	443	2	S57328	uvsh protein - Emeric	7.11e+01
42	45	86.5	477	2	S55494	CHC4 type zinc finger	7.11e+01
43	45	86.5	957	2	C59463	type I restriction-mo	7.11e+01
44	45	86.5	1999	1	S21801	myosin heavy chain, n	7.11e+01
45	45	86.5	2475	2	S35307	polyprotein pp220 pre	7.11e+01

ALIGNMENTS

RESULT	ENTRY	TITLE	12WG	#type complete
1	12WG	parathyroid hormone 4	37	mutant N-TERMINAL SUCCINYLATED -
1	12WG	synthetic		
ALTERNATE_NAMES		n-succinyl-hpch(4-37)		
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM		#formal_name synthetic		
REFERENCE		A67743		
#authors		Roesch, P.; Marx, U.C.		
#submission		submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references		PDB:12WG		
REFERENCE		TN003319		
#authors		Marx, U.C.		
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996		
COMMENT		Resolution: not applicable		
COMMENT		determination: NMR		
KEYWORDS		disease mutation; hormone; signal		
FEATURE				
2-9				
15-25				
SUMMARY		#region helix (right hand alpha)\		
		#region helix (right hand alpha)		
		#length 34 #molecular-weight 4128 #checksum 5508		
Query Match		100.0%; Score 52; DB 5; Length 34;		
Best Local Similarity		100.0%; Pred. No. 4.07e+00;		
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	21	LRKRLQD 27		
Qy	1	LRKRLQD 7		
RESULT	2	12WF	#type complete	
ENTRY		parathyroid hormone 4	37	mutant N-TERMINAL ACETYLATED -
TITLE		synthetic		
ALTERNATE_NAMES		n-acetyl-1pch(4-37)		
PDB_TITLE		structure of n-terminal acetylated human parathyroid hormone,		
ORGANISM		NMR, 10 structures		
REFERENCE		#formal_name synthetic		
REFERENCE		A67742		
#authors		Roesch, P.; Marx, U.C.		
#submission		submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references		PDB:12WF		
REFERENCE		TN003318		
#authors		Marx, U.C.		
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung,		

Thu Jul 30 13:38:16 1998

US-08-817-547A-34.rpt

Page 2

pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 52; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.07e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 21 LRKRLD 27
QY 1 LRKRLD 7

Search completed: Thu Jul 30 11:19:55 1998
Job time : 27 secs.

MUSE RELEASE

(TM)

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Search_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:18:09 1998; MasPar time 2.07 Seconds
Tabular output not generated. 84.981 Million cell updates/sec

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRKRLQD 7

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.054; Variance 26.515; scale 0.869

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	52	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	6.49e-01
2	52	100.0	115	1	PTHY_CANPA PARATHYROID HORMONE PR	6.49e-01
3	52	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	6.49e-01
4	52	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	6.49e-01
5	52	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	6.49e-01
6	48	92.3	621	1	Y04E_MYCTU HYPOTHETICAL 69.2 KD P	4.84e+00
7	47	90.4	154	1	Y17K_SSV1 HYPOTHETICAL 17.8 KD P	7.85e+00
8	46	88.5	100	1	Y191_ECOLI INSERTION ELEMENT 1591	1.26e+01
9	46	88.5	112	1	Y191_SHIDY INSERTION ELEMENT 1591	1.26e+01
10	46	88.5	224	1	TCTD_SALTY TRANSCRIPTIONAL REGULA	1.26e+01
11	46	88.5	447	1	KCC2_YEAST CALCIUM/CALMODULIN-DEP	1.26e+01
12	46	88.5	509	1	CPT7_PIG CYTOCHROME P450 XVTAL	1.26e+01
13	46	88.5	637	1	PTMA_ECOLI PTS SYSTEM, MANNITOL-S	1.26e+01
14	46	88.5	745	1	KATC_ARATH KINESIN-LIKE PROTEIN B	1.26e+01
15	46	88.5	754	1	KATC_ARATH KINESIN-LIKE PROTEIN C	1.26e+01
16	46	88.5	793	1	KATA_ARATH KINESIN-LIKE PROTEIN A	1.26e+01
17	46	88.5	806	1	SYF8_MYCGE PHENYLALANYL-TRNA SYN	1.26e+01
18	46	88.5	1231	1	KIF4_MOUSE KINESIN-LIKE PROTEIN K	1.26e+01
19	46	88.5	2492	1	POLN_EEVTY NONSTRUCTURAL POLYPEPT	1.26e+01
20	46	88.5	2492	1	POLN_EEVTY NONSTRUCTURAL POLYPEPT	1.26e+01
21	46	88.5	2492	1	POLN_EEVTY NONSTRUCTURAL POLYPEPT	1.26e+01
22	45	86.5	229	1	YXDJ_BACSU HYPOTHETICAL 26.6 KD S	2.02e+01
23	45	86.5	428	1	GFAP_BOVIN GLIAL FIBRILLARY ACIDI	2.02e+01

Result	ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	P01268;					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	ETHERIA; ARTIODACTYLA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 80056617.					
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,					
RA	POTTS J.T., JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 82037785.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 83105964.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RN	[5]					
RP	SEQUENCE OF 26-115.					
RX	MEDLINE; 74142666.					
RA	HAMILTON J.W., NITAL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,					
RA	COHN D.V.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).					
RN	[6]					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE; 71076162.					
RA	NATAL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DANSON B.F.,					
RA	AORBACH G.D., POTTS J.T. JR.;					
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).					
RN	[7]					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE; 71063634.					

Search completed: Thu Jul 30 11:18:16 1998
Job time : 7 secs.

RA BREWER H. B. JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
DEFTOS L.J., DAMSON B.F., HOGAN M.L., AURBACH G.D.;
PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
RL -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC -1- BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: V00106; 685; -.
DR EMBL: J00023; G163641; -.
DR EMBL: J00024; G163643; -.
DR EMBL: J00024; E18249; ALT-SEQ.
DR EMBL: J00024; E18250; ALT-INIT.
DR EMBL: K01938; G163647; -.
DR EMBL: M25082; G163645; -.
DR PIR: A01334; PTBO
DR PIR: A24949; A24949
DR PROSITE: PS00335; PARATHYROID; 1.
RN HORMONE; SIGNAL.
CC SIGNAL 1 25
FT PROPEP 26 31 PARATHYROID HORMONE.
FT CHAIN 32 115 V -> G (IN REF. 4).
FT CONFLICT 106 106
SO SEQUENCE 115 AA; 12980 MW; 673E5F2 CRC32;

Query Match 100.0%; Score 52; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.49e-01; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Db 55 LKRIOD 61
|||
OY 1 LKRIOD 7

RESULT 2
ID PTH CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANT'S FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
RN [1]
RN SEQUENCE FROM N.A.
RN TISSUE-PARATHYROID;
RA MEDLINE: 95369696.
RA ROSOL T.J., STEINMEYER C.L., MCCADLEY L.K., GRONE A.,
DEWILLE J.W., CAPEN C.C.;
RA GENE 160-241-243(1995).
RL -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC -1- BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: U15662; G358916; -.
DR PROSITE: PS00335; PARATHYROID; 1.
DR HORMONE; SIGNAL.
KW SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SO SEQUENCE 115 AA; 12957 MW; 16D0EBC CRC32;

Query Match 100.0%; Score 52; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.49e-01; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Db 55 LKRIOD 61
|||
OY 1 LKRIOD 7

M O S E R H
(TM)

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:18:33 1998; Maspar time 3.62 Seconds
81.362 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRRKLOD 7

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.212; Variance 26.174; scale 0.849

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	52	100.0	105	10	063473	PARATHYROID HORMONE (F	8.70e-01
2	52	100.0	929	9	032491	PUTATIVE NG-ADENINE S	1.46e+00
3	51	98.1	242	8	040970	PUTATIVE MADS-BOX FAMI	1.46e+00
4	51	98.1	242	8	P93468	MADS-BOX FAMILY TRANSC	1.46e+00
5	51	98.1	257	8	Q40700	BOX PROTEIN.	1.46e+00
6	48	92.3	398	8	004471	SIMILAR TO SACCAROMYC	6.55e+00
7	48	92.3	481	3	018255	COSMID C2709.	6.55e+00
8	47	90.4	133	9	P73817	HYPOHETICAL 15.4 KD P	1.07e+01
9	47	90.4	245	8	Q40969	PUTATIVE MADS-BOX FAMI	1.07e+01
10	47	90.4	360	9	029516	DNA PRIMASE, PUTATIVE.	1.07e+01
11	47	90.4	836	10	063618	ESPIN.	1.07e+01
12	46	88.5	122	9	P71288	HYPOHETICAL 15.4 KD P	1.72e+01
13	46	88.5	122	9	032286	XYZC PROTEIN.	1.72e+01
14	46	88.5	134	9	P75679	FROM BASES 263572 TO 2	1.72e+01
15	46	88.5	231	1	005436	CAM KINASE II (FRAGMENT	1.72e+01
16	46	88.5	263	9	P96187	HRPG.	1.72e+01
17	46	88.5	316	9	Q56689	TRANSMEMBRANE TRANSCR	1.72e+01
18	46	88.5	434	1	P78918	FISSION YEAST (FRAGMENT	1.72e+01
19	46	88.5	899	1	006132	CHROMOSOME XII COSMID	1.72e+01
20	46	88.5	1034	3	017117	M51.4 PROTEIN.	1.72e+01

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	100.0%	Score 52; DB 10; Length 105;					
2	063473	100.0%	Score 52; DB 10; Length 105;					
3	063473	100.0%	Score 52; DB 10; Length 105;					
4	063473	100.0%	Score 52; DB 10; Length 105;					
5	063473	100.0%	Score 52; DB 10; Length 105;					
6	063473	100.0%	Score 52; DB 10; Length 105;					
7	063473	100.0%	Score 52; DB 10; Length 105;					
8	063473	100.0%	Score 52; DB 10; Length 105;					
9	063473	100.0%	Score 52; DB 10; Length 105;					
10	063473	100.0%	Score 52; DB 10; Length 105;					
11	063473	100.0%	Score 52; DB 10; Length 105;					
12	063473	100.0%	Score 52; DB 10; Length 105;					
13	063473	100.0%	Score 52; DB 10; Length 105;					
14	063473	100.0%	Score 52; DB 10; Length 105;					
15	063473	100.0%	Score 52; DB 10; Length 105;					
16	063473	100.0%	Score 52; DB 10; Length 105;					
17	063473	100.0%	Score 52; DB 10; Length 105;					
18	063473	100.0%	Score 52; DB 10; Length 105;					
19	063473	100.0%	Score 52; DB 10; Length 105;					
20	063473	100.0%	Score 52; DB 10; Length 105;					

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	100.0%	Score 52; DB 10; Length 105;					
2	063473	100.0%	Score 52; DB 10; Length 105;					
3	063473	100.0%	Score 52; DB 10; Length 105;					
4	063473	100.0%	Score 52; DB 10; Length 105;					
5	063473	100.0%	Score 52; DB 10; Length 105;					
6	063473	100.0%	Score 52; DB 10; Length 105;					
7	063473	100.0%	Score 52; DB 10; Length 105;					
8	063473	100.0%	Score 52; DB 10; Length 105;					
9	063473	100.0%	Score 52; DB 10; Length 105;					
10	063473	100.0%	Score 52; DB 10; Length 105;					
11	063473	100.0%	Score 52; DB 10; Length 105;					
12	063473	100.0%	Score 52; DB 10; Length 105;					
13	063473	100.0%	Score 52; DB 10; Length 105;					
14	063473	100.0%	Score 52; DB 10; Length 105;					
15	063473	100.0%	Score 52; DB 10; Length 105;					
16	063473	100.0%	Score 52; DB 10; Length 105;					
17	063473	100.0%	Score 52; DB 10; Length 105;					
18	063473	100.0%	Score 52; DB 10; Length 105;					
19	063473	100.0%	Score 52; DB 10; Length 105;					
20	063473	100.0%	Score 52; DB 10; Length 105;					

Thu Jul 30 13:38:16 1998

US-08-817-547A-34.rspc

Page 2

RA ROD J.I.
RL MICROBIOLOGY 141:0-0(0).
DR EMBL: U20247; G2317805; -
KW TRANSFERASE; METHYLTRANSFERASE.
SQ SEQUENCE 929 AA; 1064/4 MW; 4085E117 CRC32;

Query Match 100.0%; Score 52; DB 9; Length 929;
Best Local Similarity 100.0%; Pred. No. 8.70e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 LRRKLOD 48
OY 1 LRRKLOD 7

Search completed: Thu Jul 30 11:19:10 1998
Job time : 37 secs.

KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 OS Synthetic.

PN GB2269176-A.
 PD 02-FEB-1994.
 PF 12-JUL-1993; 014384.
 PR 15-JUL-1992; GB-015009.
 PR 18-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 23-DEC-1992; GB-026861.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PA Albert R, Bauer W, Breckenridge R, Cardinaux F,
 Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 Waelchli R, Rainer A;
 DR WPI; 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 PS Example 30; Page 36; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 39; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.76e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 LrKkL 28
 QY 1 LrKkL 5

Search completed: Thu Jul 30 11:22:55 1998
 Job time : 15 secs.

W D S E I F

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Search_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:22:05 1998; Maspar time 2.97 Seconds
Tabular output not generated. 61.502 Million cell updates/sec

Title: >US-08-817-547A-36
Description: (1-5) from US08817547A.pep
Perfect Score: 39
Sequence: 1 LRKKL 5

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

plrs56
1:plrl 2:plrl2 3:plrl3 4:plrl4 5:nlrl3d

Statistics: Mean 20.005; Variance 26.164; scale 0.765

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Suit No.	Score	Query Match	Length	ID	Description	Pred. No.
1	39	100.0	34	5	12WE parathyroid hormone (1.53e+02
2	39	100.0	34	5	12WG parathyroid hormone 4	1.53e+02
3	39	100.0	34	5	12WH cyclic parathyroid ho	1.53e+02
4	39	100.0	34	5	12WA parathyroid hormone (1.53e+02
5	39	100.0	34	5	12WF parathyroid hormone 4	1.53e+02
6	39	100.0	35	5	12WD parathyroid hormone (1.53e+02
7	39	100.0	36	5	12WB parathyroid hormone (1.53e+02
8	39	100.0	37	5	12HP parathyroid hormone f	1.53e+02
9	39	100.0	37	5	12WC parathyroid hormone (1.53e+02
10	39	100.0	73	5	3FISA F1s protein (factor f	1.53e+02
11	39	100.0	73	5	3FISA DNA-binding protein f	1.53e+02
12	39	100.0	73	5	3FISB F1s protein (factor f	1.53e+02
13	39	100.0	74	5	1F1AB F1s protein (factor f	1.53e+02
14	39	100.0	75	5	1F1AB2 F1s protein (factor f	1.53e+02
15	39	100.0	89	5	1F1AA2 F1s protein (factor f	1.53e+02
16	39	100.0	89	5	1F36B F1s mutant K36E, cha	1.53e+02
17	39	100.0	271	5	1RUPA2 rhinovirus 14 mutant	1.53e+02
18	39	100.0	273	5	1RUCV rhinovirus 14 mutant	1.53e+02
19	39	100.0	273	5	1HRVA rhinovirus 14 (hrv14)	1.53e+02
20	39	100.0	273	5	1RUGA rhinovirus 14 mutant	1.53e+02
21	39	100.0	273	5	1RUGA rhinovirus 14 mutant	1.53e+02
22	39	100.0	273	5	1RHIA rhinovirus 3 coat pro	1.53e+02
23	39	100.0	273	5	1VRHA rhinovirus 14 mutant	1.53e+02

24	39	100.0	273	5	1RUEA rhinovirus 14 mutant	1.53e+02
25	39	100.0	273	5	1RUDA rhinovirus 14 mutant	1.53e+02
26	39	100.0	273	5	1RUGA rhinovirus 14 mutant	1.53e+02
27	39	100.0	273	5	2R07A coat protein VP1 (wit	1.53e+02
28	39	100.0	273	5	2R81A coat protein VP1 (wit	1.53e+02
29	39	100.0	273	5	2R2A coat protein VP1 (wit	1.53e+02
30	39	100.0	273	5	4RIVA coat protein VP1, chta	1.53e+02
31	39	100.0	273	5	2R5A coat protein VP1 (wit	1.53e+02
32	39	100.0	273	5	2R53A coat protein VP1 (wit	1.53e+02
33	39	100.0	273	5	2R6A coat protein VP1 (wit	1.53e+02
34	39	100.0	273	5	2HMB coat protein VP1 muta	1.53e+02
35	39	100.0	273	5	1R09A coat protein VP1 (wit	1.53e+02
36	39	100.0	273	5	2R04A coat protein VP1 (wit	1.53e+02
37	39	100.0	273	5	2HWCA coat protein VP1 muta	1.53e+02
38	39	100.0	273	5	2RRIA coat protein VP1 (wit	1.53e+02
39	39	100.0	273	5	1RUIA rhinovirus 14 mutant	1.53e+02
40	39	100.0	273	5	1HRIA coat protein VP1 (wit	1.53e+02
41	39	100.0	273	5	1R08A coat protein VP1 (wit	1.53e+02
42	39	100.0	492	5	1ECGA glutamine phosphoribo	1.53e+02
43	39	100.0	492	5	1ECFA glutamine phosphoribo	1.53e+02
44	39	100.0	500	5	1ECFB glutamine phosphoribo	1.53e+02
45	39	100.0	500	5	1ECGB glutamine phosphoribo	1.53e+02

ALIGNMENTS

RESULT 1
ENTRY 12WE #type complete
TITLE parathyroid hormone (residues 4-37) - human
PDB-TITLE HPTH(4-37)
PDB-TITLE structure of human parathyroid hormone fragment 4-37, NMR 10 structures
ORGANISM #formal_name Homo sapiens #common_name man
REFERENCE A67860
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WE
REFERENCE TN001721
#authors Marx, U.C.
#book In: Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
KEYWORDS Determination: NMR
FEATURE hormone
SUMMARY #region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 39; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.53e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 21 LRKKL 25
Qy 1 LRKKL 5
RESULT 2
ENTRY 12WG #type complete
TITLE parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -
PDB-TITLE n-succinyl-hPTH(4-37)
PDB-TITLE succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM #formal_name synthetic
REFERENCE A67743
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WG
REFERENCE TN003319
#authors Marx, U.C.
#book In: Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable

Thu Jul 30 13:38:16 1998

US-08-817-547A-36.rpr

Page 2

COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE 2-9
15-25 #region helix (right hand alpha)\
SUMMARY #region helix (right hand alpha)
#length 34 #molecularweight 4128 #checksum 5508
Query Match 100.0%; Score 39; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.53e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 21 LRRKL 25
OY 1 LRRKL 5

Search completed: Thu Jul 30 11:22:22 1998
Job time : 17 secs.

MISCELLANEOUS

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:20:45 1998; Maspar time 2.01 Seconds
Tabular output not generated. 62.459 Million cell updates/sec

Title: >US-08-817-547A-36
Description: (1-5) from US08817547A.pep
Perfect Score: 39
Sequence: 1 LRKL 5

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 21.052; Variance 21.024; scale 1.001

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Hit No.	Score	Query Length	ID	Description	Pred. No.
1	39	100.0	98	1 FIS_ECOLI FACTOR-FOR-INVERSION S	4.38e+01
2	39	100.0	100	1 Y191_ECOLI INSERTION ELEMENT 1S91	4.38e+01
3	39	100.0	112	1 Y191_SHIDY INSERTION ELEMENT 1S91	4.38e+01
4	39	100.0	115	1 PTHY_CANPA PARATHYROID HORMONE PR	4.38e+01
5	39	100.0	115	1 PTHY_HUMAN PARATHYROID HORMONE PR	4.38e+01
6	39	100.0	115	1 PTHY_BOVIN PARATHYROID HORMONE PR	4.38e+01
7	39	100.0	209	1 VSI0_ROTBS MINOR OUTER CAPSID PRO	4.38e+01
8	39	100.0	209	1 RR3_GRATE CHLOROPLAST 30S RIBOSO	4.38e+01
9	39	100.0	213	1 URK_MYCPN URIDINE KINASE (EC 2.7	4.38e+01
10	39	100.0	224	1 TCTD_SALTY TRANSCRIPTIONAL REGULA	4.38e+01
11	39	100.0	229	1 YXDU_BACSU HYPOTHEICAL 26.6 KD S	4.38e+01
12	39	100.0	242	1 RSTA_ECOLI TRANSCRIPTIONAL REGULA	4.38e+01
13	39	100.0	310	1 SYNK_ARATH SYNTAXIN-RELATED PROTE	4.38e+01
14	39	100.0	330	1 YXAO_BACSU HYPOTHEICAL 37.5 KD P	4.38e+01
15	39	100.0	334	1 YH05_YEAST HYPOTHEICAL 37.9 KD P	4.38e+01
16	39	100.0	353	1 V613_MERJA PUTATIVE ENDONUCLEASE	4.38e+01
17	39	100.0	360	1 HIS8_LACIA HISTIDINOL-PHOSPHATE A	4.38e+01
18	39	100.0	366	1 STY_SULSO TYROSYL-TRNA SYNTHETAS	4.38e+01
19	39	100.0	435	1 MRP_MYCLE MRP PROTEIN HOMOLOG.	4.38e+01
20	39	100.0	437	1 SECY_STRGB PREPROTEIN TRANSLOCASE	4.38e+01
21	39	100.0	437	1 SECY_STRGR PREPROTEIN TRANSLOCASE	4.38e+01
22	39	100.0	437	1 SECY_STRSC PREPROTEIN TRANSLOCASE	4.38e+01
23	39	100.0	437	1 SECT_STRLI PREPROTEIN TRANSLOCASE	4.38e+01

RESULT	1	STANDARD;	PRT;	98 AA.
ID	FIS_ECOLI			
AC	P11028: P37404:			
DT	01-JUL-1989 (REL. 11, CREATED)			
DT	01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	FACTOR-FOR-INVERSION STIMULATION PROTEIN (HIN RECOMBINATIONAL ENHANCER			
DE	DE BINDING PROTEIN) (FIS PROTEIN).			
GN	FIS.			
OS	ESCHERICHIA COLI, AND SALMONELLA TYPHIMURUM.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
OC	ENTEROBACTERIACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 88217925.			
RA	JOHNSON R.C., BALL C.A., PFEFFER D., SIMON M.I.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 85:3484-3488(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 88247997.			
RA	KOCH C., VANDERKERCKHOVE J., KAHMANN R.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 85:4237-4241(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 93094136.			
RA	BALL C.A., OSUNA R., PERCUSON K.C., JOHNSON R.C.;			
RL	J. BACTERIOL. 174:8043-8056(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-E.COLI: STRAIN-K12 / MG1655:			
RA	BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;			
RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-S.TYPHIMURUM: STRAIN-LT2;			
RX	MEDLINE: 95238273.			
RA	OSUNA R., LIENAU D., HUGHES K.T., JOHNSON R.C.;			
RL	J. BACTERIOL. 177:2021-2032(1995).			
RN	[6]			
RP	FUNCTION.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 91006075.			
RA	ROSS W., THOMPSON J.F., NEWLANDS J.T., GOURSE R.L.;			
RL	EMBO J. 9:3733-3742(1990).			

24	39	100.0	444	1 PURA_STYV3 ADENYLOSUCINATE SYNTH	4.38e+01
25	39	100.0	451	1 TRPC_BUCAP INDOLE-3-GLYCEROL PHOS	4.38e+01
26	39	100.0	455	1 YNU6_YEAST HYPOTHEICAL 51.6 KD P	4.38e+01
27	39	100.0	459	1 NUT4M_HYLLA NADH-UBIQUINONE OXIDOR	4.38e+01
28	39	100.0	479	1 ICE8_HUMAN CASPASE-8 PRECURSOR (E	4.38e+01
29	39	100.0	496	1 SRM_MOUSE TYROSINE-PROTEIN KINAS	4.38e+01
30	39	100.0	496	1 RECO_BACSU ATP-DEPENDENT DNA HELI	4.38e+01
31	39	100.0	501	1 UVS2_NEUCR UVS-2 PROTEIN.	4.38e+01
32	39	100.0	504	1 PUR1_ECOLI AMIDOPHOSPHORIBOSYLTRA	4.38e+01
33	39	100.0	517	1 PUR1_HUMAN AMIDOPHOSPHORIBOSYLTRA	4.38e+01
34	39	100.0	517	1 PUR1_HUMAN AMIDOPHOSPHORIBOSYLTRA	4.38e+01
35	39	100.0	744	1 NUB3_YEAST NUCLEOPORIN NUP85 (NUC	4.38e+01
36	39	100.0	745	1 KATB_ARATH KINESIN-LIKE PROTEIN B	4.38e+01
37	39	100.0	754	1 KATC_ARATH KINESIN-LIKE PROTEIN C	4.38e+01
38	39	100.0	800	1 RR3_CHLEU CHLOROPLAST PUTATIVE 3	4.38e+01
39	39	100.0	806	1 SYEB_MYGE PHENYLAANYL-TRNA SYN	4.38e+01
40	39	100.0	926	1 POOL_HAFTN PROBABLE ZINC PROTEASE	4.38e+01
41	39	100.0	1031	1 RAD2_YEAST DNA REPAIR PROTEIN RAD	4.38e+01
42	39	100.0	1032	1 YQ53_CAEEL HYPOTHEICAL 117.1 KD	4.38e+01
43	39	100.0	2492	1 POLN_EEYVP NONSTRUCTURAL POLYPROT	4.38e+01
44	39	100.0	2492	1 POLN_EEYV3 NONSTRUCTURAL POLYPROT	4.38e+01
45	39	100.0	2492	1 POLN_EEYVT NONSTRUCTURAL POLYPROT	4.38e+01

RN [7]
RP FUNCTION.
RX MEDLINE; 96433150.
RA WOLD S., CROOKE E., SKARSTAD K.;
RL NUCLEIC ACIDS RES. 24:3527-3532(1996).
RN [8]
RP MUTAGENESIS, AND DOMAINS.
RC SPECIES-E.COLI;
RX MEDLINE; 9122411.
RA OSUNA R., FINKEL S.E., JOHNSON R.C.;
RL EMOB J. 10:1593-1603(1991).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES-E.COLI;
RX MEDLINE; 91095026.
RA KOSTREWA D., GRANZIN J., KOCH C., CHOE H.-W., RAGHUNATHAN S., WOLF W.,
RA LABAHN J., KAHNANN R., SAENGER W.;
RL NATURE 349:178-180(1991).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES-E.COLI;
RX MEDLINE; 92318262.
RA KOSTREWA D., GRANZIN J., STOCK D., CHOE H.-W., LABAHN J., SAENGER W.;
RL J. MOL. BIOL. 226:209-226(1992).
CC -1- FUNCTION: ACTIVATES RIBOSOMAL RNA TRANSCRIPTION. PLAYS A DIRECT
CC ROLE IN UPSTREAM ACTIVATION OF RNA PROMOTERS. BINDS TO A
CC RECOMBINATIONL ENHANCER SEQUENCE THAT IS REQUIRED TO STIMULATE
CC HIN-MEDIATED DNA INVERSION. PREVENTS INITIATION OF DNA REPLICATION
CC FROM ORIC.
CC -1- SUBUNIT: HOMODIMER.
DR EMBL; J03245; G145971; -;
DR EMBL; J03816; G145973; -;
DR EMBL; M95784; G145977; -;
DR EMBL; U18987; G606202; -;
DR EMBL; AE000405; G1789661; -;
DR PIR; A32142; DNECRS.
DR PIR; A28207; A28207.
DR PIR; S15344; S15344.
DR PIR; C47043; C47043.
DR PDB; 1F7A; 31-OCT-93.
DR PDB; 1F7P; 14-FEB-95.
DR PDB; 3FIS; 31-OCT-93.
DR PDB; 4FIS; 31-OCT-93.
DR ECGENE; EG10317; FIS.
DR STYGENE; SG10100; FIS.
KW DNA-BINDING; 3D-STRUCTURE.
FT DOMAIN 17 44
FT DNA_BIND 74 93
FT HELIX 27 40
FT TURN 41 41
FT TURN 43 44
FT TURN 50 70
FT TURN 71 72
FT HELIX 74 81
FT TURN 82 82
FT HELIX 85 94
FT TURN 95 96
SQ SEQUENCE 98 AA; 11240 MW; 6AE88082 CRC32;
Query Match 100.0%; Score 39; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.38e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 88 LRKRL 92
QY 1 LRKRL 5
RESULT 2
ID Y191_ECOLI STANDARD; PRT; 100 AA.
AC P39212;

DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE INSERTION ELEMENT 18911 HYPOTHETICAL 11.6 KD PROTEIN (O100).
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 95334362.
RA BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
RA BLATTNER F.R.;
RL NUCLEIC ACIDS RES. 23:2105-2119(1995).
DR EMBL; U14003; G537124; -;
DR EMBL; AE000499; G1790735; -;
KW HYPOTHETICAL PROTEIN; TRANSDUCIBLE ELEMENT.
SQ SEQUENCE 100 AA; 11558 MW; 3827E6B9 CRC32;
Query Match 100.0%; Score 39; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.38e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 82 LRKRL 86
QY 1 LRKRL 5
Search completed: Thu Jul 30 11:20:51 1998
Job time : 6 secs.

Thu Jul 30 13:38:17 1998

US-08-817-547A-36.ispt

Page 2

DR EMBL: M54875; G601933; -
FT NON_TER 1
SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;

Query Match 100.0%; Score 39; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.95e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 LKKL 49
1 LKKL 5
Qy 1 LKKL 5

Search completed: Thu Jul 30 11:21:47 1998
Job time : 37 secs.